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<p>(54) Title: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS</p> <p>(57) Abstract</p> <p>The invention provides human signal peptide-containing proteins (HSPP) and polynucleotides which identify and encode HSPP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of HSPP.</p>																																								

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HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

5

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human signal peptide-containing proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative disorders including cancer, inflammation, and cardiovascular, neurological, reproductive, and developmental disorders.

BACKGROUND OF THE INVENTION

Protein transport is essential for cellular function. Transport of a protein may be mediated by a signal peptide located at the amino terminus of the protein itself. The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the nascent protein from the ribosome to a particular membrane bound compartment such as the endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes. Proteins that transit through the secretory pathway are either secreted into the extracellular space or retained in the plasma membrane. Secreted proteins are often synthesized as inactive precursors that are activated by post-translational processing events during transit through the secretory pathway. Such events include glycosylation, phosphorylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that may occur during protein transport include chaperone-dependent unfolding and folding of the nascent protein and interaction of the protein with a receptor or pore complex. Examples of secreted proteins with amino terminal signal peptides are discussed below and include receptors, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuropeptides, vasomediators, phosphokinases, phosphatases, phospholipases, phosphodiesterases, G and Ras-related proteins, ion channels, transporters/pumps, proteases, and transcription factors. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 557-560, 582-592.)

G-protein coupled receptors (GPCRs) comprise a superfamily of integral membrane proteins which transduce extracellular signals. GPCRs include receptors for biogenic amines such as dopamine, epinephrine, histamine, glutamate (metabotropic effect), acetylcholine (muscarinic effect), and serotonin; for lipid mediators of inflammation such as prostaglandins, platelet activating factor, and leukotrienes; for peptide hormones such as calcitonin, C5a anaphylatoxin, follicle stimulating hormone, gonadotropin releasing hormone, neurokinin, oxytocin, and thrombin; and for sensory signal mediators such as retinal photopigments and olfactory stimulatory molecules. The structure of these highly conserved receptors consists of seven hydrophobic transmembrane regions, cysteine disulfide bridges between the second and third extracellular loops, an extracellular N-terminus, and a cytoplasmic C-terminus. The N-terminus interacts with ligands, the disulfide bridges interact with agonists and antagonists, and the large third intracellular loop interacts with G proteins to activate second messengers such as cyclic AMP, phospholipase C, inositol triphosphate, or ion channels. (Reviewed in Watson, S. and Arkininstall, S. (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego, CA, pp. 2-6; and Bolander, F.F. (1994) Molecular Endocrinology, Academic Press, San Diego, CA, pp. 162-176.)

Other types of receptors include cell surface antigens identified on leukocytic cells of the immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into "clusters of differentiation" based on common immunocytochemical localization patterns in various differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a "CD" number. Some of the genes encoding proteins identified by CD antigens have been isolated and characterized as both transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed in Barclay, A. N. et al. (1993) The Leucocyte Antigen Facts Book, Academic Press, San Diego, CA, pp. 144-145; Noel, L. S. et al. (1998) J. Biol. Chem. 273:3878-3883.)

Tetraspanins are a superfamily of membrane proteins which facilitate the formation

and stability of cell-surface signaling complexes containing lineage-specific proteins, integrins, and other tetraspanins. They are involved in cell activation, proliferation (including cancer), differentiation, adhesion, and motility. These proteins cross the membrane four times, have conserved intracellular – and C-termini and an extracellular, non-conserved hydrophilic domain. Tetraspanins include, e.g., platelet and endothelial cell membrane proteins, leukocyte surface proteins, tissue specific and tumorous antigens, and the retinitis pigmentosa-associated gene peripherin. (Maecker, H.T. et al. (1997) FASEB J. 11:428-442.)

Matrix proteins (MPs) are transmembrane and extracellular proteins which function in formation, growth, remodeling, and maintenance of tissues and as important mediators and regulators of the inflammatory response. The expression and balance of MPs may be perturbed by biochemical changes that result from congenital, epigenetic, or infectious diseases. In addition, MPs affect leukocyte migration, proliferation, differentiation, and activation in the immune response. MPs are frequently characterized by the presence of one or more domains which may include collagen-like domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition, some MPs are heavily glycosylated. MPs include extracellular proteins such as fibronectin, collagen, and galectin and cell adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed in Ayad, S. et al. (1994) The Extracellular Matrix Facts Book, Academic Press, San Diego, CA, pp. 2-16; Ruoslahti, E. (1997) *Kidney Int.* 51:1413-1417; Sjaastad, M.D. and Nelson, W.J. (1997) *BioEssays* 19:47-55.)

Lectins are proteins characterized by their ability to bind carbohydrates on cell membranes by means of discrete, modular carbohydrate recognition domains, CRDs. (Kishore, U. et al. (1997) *Matrix Biol.* 15:583-592.) Certain cytokines and membrane-spanning proteins have CRDs which may enhance interactions with extracellular or intracellular ligands, with proteins in secretory pathways, or with molecules in signal transduction pathways. The lipocalin superfamily constitutes a phylogenetically conserved group of more than forty proteins that function by binding to and transporting a variety of physiologically important ligands. (Tanaka, T. et al. (1997) *J. Biol. Chem.* 272:15789-15795; and van't Hof, W. et al. (1997) *J. Biol. Chem.* 272:1837-1841.) Selectins are a family of calcium ion-dependent lectins expressed on inflamed vascular

endothelium and the surface of some leukocytes. (Rossiter, H. et al. (1997) Mol. Med. Today 3:214-222.)

Protein kinases regulate many different cell proliferation, differentiation, and signaling processes by adding phosphate groups to proteins. Reversible protein phosphorylation is a key strategy for controlling protein functional activity in eukaryotic cells. The high energy phosphate which drives this activation is generally transferred from adenosine triphosphate molecules (ATP) to a particular protein by protein kinases and removed from that protein by protein phosphatases. Phosphorylation occurs in response to extracellular signals, cell cycle checkpoints, and environmental or nutritional stresses.

Protein kinases may be roughly divided into two groups; protein tyrosine kinases (PTKs) which phosphorylate tyrosine residues, and serine/threonine kinases (STKs) which phosphorylate serine or threonine residues. A few protein kinases have dual specificity. A majority of kinases contain a similar 250-300 amino acid catalytic domain. (Hardie, G. and Hanks, S. (1995) The Protein Kinase Facts Book, Vol I, pp. 7-47, Academic Press, San Diego, CA.)

Protein phosphatases remove phosphate groups from molecules previously modified by protein kinases thus participating in cell signaling, proliferation, differentiation, contacts, and oncogenesis. Protein phosphorylation is a key strategy used to control protein functional activity in eukaryotic cells. The high energy phosphate is transferred from ATP to a protein by protein kinases and removed by protein phosphatases. There appear to be three, evolutionarily-distinct protein phosphatase gene families: protein phosphatases (PPs); protein tyrosine phosphatases (PTPs); and acid/alkaline phosphatases (APs). PPs dephosphorylate phosphoserine/threonine residues and are an important regulator of many cAMP mediated, hormone responses in cells.

PTPs reverse the effects of protein tyrosine kinases and therefore play a significant role in cell cycle and cell signaling processes. Although APs dephosphorylate substrates in vitro, their role in vivo is not well known. (Charbonneau, H. and Tonks, N.K. (1992) Annu. Rev. Cell Biol. 8:463-493.)

Cyclic nucleotides (cAMP and cGMP) function as intracellular second messengers to transduce a variety of extracellular signals, including hormones, light and neurotransmitters. Cyclic nucleotide phosphodiesterases (PDEs) degrade cyclic nucleotides to their corresponding monophosphates, thereby regulating the intracellular

concentrations of cyclic nucleotides and their effects on signal transduction. At least seven families of mammalian PDEs have been identified based on substrate specificity and affinity, sensitivity to cofactors and sensitivity to inhibitory drugs. (Beavo, J.A. (1995) *Physiological Reviews* 75: 725-748.)

5 Phospholipases (PLs) are enzymes that catalyze the removal of fatty acid residues from phosphoglycerides. PLs play an important role in transmembrane signal transduction and are named according to the specific ester bond in phosphoglycerides that is hydrolyzed, i.e., A₁, A₂, C or D. PLA₂ cleaves the ester bond at position 2 of the glycerol moiety of membrane phospholipids giving rise to arachidonic acid. Arachidonic acid is
10 the common precursor to four major classes of eicosanoids, namely prostaglandins, prostacyclins, thromboxanes and leukotrienes. Eicosanoids are signaling molecules involved in the contraction of smooth muscle, platelet aggregation, and pain and inflammatory responses. (Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, Inc., New York, NY, pp. 85, 211, 239-240, 642-645.)

15 The nucleotide cyclases, i.e., adenylate and guanylate cyclase, catalyze the synthesis of the cyclic nucleotides, cAMP and cGMP, from ATP and GTP, respectively. They act in concert with phosphodiesterases, which degrade cAMP and cGMP, to regulate the cellular levels of these molecules and their functions. cAMP and cGMP function as intracellular second messengers to transduce a variety of extracellular signals, e.g.,
20 hormones, and light and neurotransmitters. (Stryer, L. (1988) Biochemistry W.H. Freeman and Co., New York, pp. 975-980, 1029-1035.)

 Cytokines are produced in response to cell perturbation. Some cytokines are produced as precursor forms, and some form multimers in order to become active. They are produced in groups and in patterns characteristic of the particular stimulus or disease,
25 and the members of the group interact with one another and other molecules to produce an overall biological response. Interleukins, neurotrophins, growth factors, interferons, and chemokines are all families of cytokines which work in conjunction with cellular receptors to regulate cell proliferation and differentiation and to affect such activities as leukocyte migration and function, hematopoietic cell proliferation, temperature regulation, acute
30 response to infections, tissue remodeling, apoptosis, and cell survival. Studies using antibodies or other drugs that modify the activity of a particular cytokine are used to elucidate the roles of individual cytokines in pathology and physiology.

Chemokines, in particular, are small chemoattractant cytokines involved in inflammation, leukocyte proliferation and migration, angiogenesis and angiostasis, regulation of hematopoiesis, HIV infectivity, and stimulation of cytokine secretion. Chemokines generally contain 70-100 amino acids and are subdivided into four
5 subfamilies based on the presence of conserved cysteine-based motifs. (Callard, R. and Gearing, A. (1994) The Cytokine Facts Book, Academic Press, New York, NY, pp. 181-190, 210-213, 223-227.)

Growth and differentiation factors are secreted proteins which function in intercellular communication. Some factors require oligomerization or association with
10 MPs for activity. Complex interactions among these factors and their receptors trigger intracellular signal transduction pathways that stimulate or inhibit cell division, cell differentiation, cell signaling, and cell motility. Most growth and differentiation factors act on cells in their local environment (paracrine signaling). There are three broad classes of growth and differentiation factors. The first class includes the large polypeptide growth
15 factors such as epidermal growth factor, fibroblast growth factor, transforming growth factor, insulin-like growth factor, and platelet-derived growth factor. The second class includes the hematopoietic growth factors such as the colony stimulating factors (CSFs). Hematopoietic growth factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils,
20 neutrophils, macrophages, and their stem cell precursors. The third class includes small peptide factors such as bombesin, vasopressin, oxytocin, endothelin, transferrin, angiotensin II, vasoactive intestinal peptide, and bradykinin which function as hormones to regulate cellular functions other than proliferation.

Growth and differentiation factors play critical roles in neoplastic transformation of
25 cells in vitro and in tumor progression in vivo. Inappropriate expression of growth factors by tumor cells may contribute to vascularization and metastasis of melanotic tumors. During hematopoiesis, growth factor misregulation can result in anemias, leukemias, and lymphomas. Certain growth factors such as interferon are cytotoxic to tumor cells both in vivo and in vitro. Moreover, some growth factors and growth factor receptors are related
30 both structurally and functionally to oncoproteins. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncosuppressor genes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor, MI, pp. 1-9.)

Proteolytic enzymes or proteases either activate or deactivate proteins by hydrolyzing peptide bonds. Proteases are found in the cytosol, in membrane-bound compartments, and in the extracellular space. The major families are the zinc, serine, cysteine, thiol, and carboxyl proteases.

- 5 Zinc proteases, e.g., carboxypeptidase A, have a zinc ion bound to the active site. These proteases recognize C-terminal residues that contain an aromatic or bulky aliphatic side chain, and hydrolyze the peptide bond adjacent to the C-terminal residues. Serine proteases have an active site serine residue and include digestive enzymes, e.g., trypsin and chymotrypsin, components of the complement and blood-clotting cascades, and
- 10 enzymes that control the degradation and turnover of extracellular matrix (ECM) molecules. Cysteine proteases (e.g. cathepsin) are produced by monocytes, macrophages and other immune cells, and are involved in diverse cellular processes ranging from the processing of precursor proteins to intracellular degradation. Overproduction of these enzymes can cause the tissue destruction associated with rheumatoid arthritis and asthma.
- 15 Thiol proteases, e.g., papain, contain an active site cysteine and are widely distributed within tissues. Carboxyl proteases, e.g., pepsin, are active only under acidic conditions (pH 2 to 3).

- Guanosine triphosphate-binding proteins (G proteins) can be grouped into two major classes: heterotrimeric G proteins and small G proteins. Heterotrimeric G proteins
- 20 interact with GPCRs that respond to hormones, growth factors, neuromodulators, or other signaling molecules. The interaction between GPCR and G protein allows the G protein to exchange GTP for guanosine diphosphate (GDP). This exchange activates the G protein, allowing it to dissociate from the receptor and interact with its cognate second messenger-generating protein, e.g., adenylate cyclase, guanylate cyclase, phospholipase C,
- 25 or ion channels. The hydrolysis of GTP to GDP by the G protein acts as an on-off switch, terminating the action of the G protein and preparing it to interact with another receptor molecule, thus beginning another round of signal transduction.

- The small G proteins consist of single 21-30 kDa polypeptides. They can be classified into five subfamilies: Ras, Rho, Ran, Rab, and ADP-ribosylation factor. These
- 30 proteins regulate cell growth, cell cycle control, protein secretion, and intracellular vesicle interaction. In particular, the Ras proteins are essential in transducing signals from receptor tyrosine kinases to serine/threonine kinases which control cell growth and

differentiation. Mutant Ras proteins, which bind but can not hydrolyze GTP, are permanently activated and cause continuous cell proliferation or cancer. All five subfamilies share common structural features and four conserved motifs. Most of the membrane-bound G proteins require a carboxy terminal isoprenyl group (CAAX), added posttranslationally, for membrane association and biological activity. The G proteins also have a variable effector region, located between motifs I and II, which is characterized as the interaction site for guanine nucleotide exchange factors or GTPase-activating proteins.

Eukaryotic cells are bound by a membrane and subdivided into membrane-bound compartments. Membranes are impermeable to many ions and polar molecules, therefore transport of these molecules is mediated by ion channels, ion pumps, transport proteins, or pumps. Symporters and antiporters regulate cytosolic pH by transporting ions and small molecules, e.g., amino acids, glucose, and drugs, across membranes; symporters transport small molecules and ions in the same direction, and antiporters, in the opposite direction. Transporter superfamilies include facilitative transporters and active ATP binding cassette transporters involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo conformational changes in order to transfer the ion or molecule across a membrane. Transport can occur by a passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis or an ion gradient.

Ion channels, ion pumps, and transport proteins mediate the transport of molecules across cellular membranes. Symporters and antiporters regulate cytosolic pH by transporting ions and small molecules such as amino acids, glucose, and drugs. Symporters transport small molecules and ions unidirectionally, and antiporters, bidirectionally. Transporter superfamilies include facilitative transporters and active ATP-binding cassette transporters which are involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo a conformational change in order to transfer the ion or molecule across the membrane. Transport can occur by a passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 523-546.)

Ion channels are formed by transmembrane proteins which create a lined passageway across the membrane through which water and ions, such as Na^+ , K^+ , Ca^{2+} , and Cl^- , enter and exit the cell. For example, chloride channels are involved in the regulation of the membrane electric potential as well as absorption and secretion of ions across the membrane. Chloride channels also regulate the internal pH of membrane-bound organelles.

Ion pumps are ATPases which actively maintain membrane gradients. Ion pumps are classified as P, V, or F according to their structure and function. All have one or more binding sites for ATP in their cytosolic domains. The P-class ion pumps include Ca^{2+} ATPase and Na^+/K^+ ATPase and function in transporting H^+ , Na^+ , K^+ , and Ca^{2+} ions. P-class pumps consist of two α and two β transmembrane subunits. The V- and F-class ion pumps have similar structures and but transport only H^+ . F class H^+ pumps mediate transport across the membranes of mitochondria and chloroplasts, while V-class H^+ pumps regulate acidity inside lysosomes, endosomes, and plant vacuoles.

A family of structurally related intrinsic membrane proteins known as facilitative glucose transporters catalyze the movement of glucose and other selected sugars across the plasma membrane. The proteins in this family contain a highly conserved, large transmembrane domain comprised of 12 α -helices, and several weakly conserved, cytoplasmic and exoplasmic domains (Pessin, J. E., and Bell, G.I. (1992) *Annu. Rev. Physiol.* 54:911-930).

Amino acid transport is mediated by Na^+ dependent amino acid transporters. These transporters are involved in gastrointestinal and renal uptake of dietary and cellular amino acids and in neuronal reuptake of neurotransmitters. Transport of cationic amino acids is mediated by the system y^+ family and the cationic amino acid transporter (CAT) family. Members of the CAT family share a high degree of sequence homology, and each contains 12-14 putative transmembrane domains (Ito, K. and Groudine, M. (1997) *J. Biol. Chem.* 272:26780-26786).

Proton-coupled, 12 membrane-spanning domain transporters such as PEPT 1 and PEPT 2 are responsible for gastrointestinal absorption and for renal reabsorption of peptides using an electrochemical H^+ gradient as the driving force. A heterodimeric peptide transporter, consisting of TAP 1 and TAP 2, is associated with antigen processing. Peptide antigens are transported across the membrane of the endoplasmic reticulum so

they can be presented to the major histocompatibility complex class I molecules. Each TAP protein consists of multiple hydrophobic membrane spanning segments and a highly conserved ATP-binding cassette. (Boll, M. et al. (1996) Proc. Natl. Acad. Sci. 93:284-289.)

- 5 Hormones are secreted molecules that travel through the circulation and bind to specific receptors on the surface of, or within, target cells. Although they have diverse biochemical compositions and mechanisms of action, hormones can be grouped into two categories. One category consists of small lipophilic hormones that diffuse through the plasma membrane of target cells, bind to cytosolic or nuclear receptors, and form a
- 10 complex that alters gene expression. Examples of these molecules include retinoic acid, thyroxine, and the cholesterol-derived steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category consists of hydrophilic hormones that function by binding to cell surface receptors that transduce signals across the plasma membrane. Examples of such hormones include amino acid derivatives such
- 15 as catecholamines and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotrophic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al. (1995) Molecular Cell Biology, Scientific American Books Inc., New York, NY, pp. 856-864.)
- 20 Neuropeptides and vasomediators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive intestinal peptide,
- 25 and circulatory system-borne signaling molecules such as angiotensin, complement, calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin and gastrin. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C. R. et al.
- 30 (1985) Endocrine Physiology, Oxford University Press, New York, NY, pp. 57-62.)

Regulatory molecules turn individual genes or groups of genes on and off in response to various inductive mechanisms of the cell or organism; act as transcription factors by determining

whether or not transcription is initiated, enhanced, or repressed; and splice transcripts as dictated in a particular cell or tissue. Although they interact with short stretches of DNA scattered throughout the entire genome, most gene expression is regulated near the site at which transcription starts or within the open reading frame of the gene being expressed. Many of the transcription factors incorporate one of a set of DNA-binding structural motifs, each of which contains either α helices or β sheets and binds to the major groove of DNA. (Pabo, C.O. and R.T. Sauer (1992) Ann. Rev. Biochem. 61:1053-95.) Other domains of transcription factors may form crucial contacts with the DNA. In addition, accessory proteins provide important interactions which may convert a particular protein complex to an activator or a repressor or may prevent binding. (Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing Co, New York, NY pp. 401-474.)

The discovery of new human signal peptide-containing proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders.

SUMMARY OF THE INVENTION

The invention features substantially purified polypeptides, proteins with signal peptides, referred to collectively as "HSPP" and individually as "HSPP-1", "HSPP-2", "HSPP-3", "HSPP-4", "HSPP-5", "HSPP-6", "HSPP-7", "HSPP-8", "HSPP-9", "HSPP-10", "HSPP-11", "HSPP-12", "HSPP-13", "HSPP-14", "HSPP-15", "HSPP-16", "HSPP-17", "HSPP-18", "HSPP-19", "HSPP-20", "HSPP-21", "HSPP-22", "HSPP-23", "HSPP-24", "HSPP-25", "HSPP-26", "HSPP-27", "HSPP-28", "HSPP-29", "HSPP-30", "HSPP-31", "HSPP-32", "HSPP-33", "HSPP-34", "HSPP-35", "HSPP-36", "HSPP-37", "HSPP-38", "HSPP-39", "HSPP-40", "HSPP-41", "HSPP-42", "HSPP-43", "HSPP-44", "HSPP-45", "HSPP-46", "HSPP-47", "HSPP-48", "HSPP-49", "HSPP-50", "HSPP-51", "HSPP-52", "HSPP-53", "HSPP-54", "HSPP-55", "HSPP-56", "HSPP-57", "HSPP-58", "HSPP-59", "HSPP-60", "HSPP-61", "HSPP-62", "HSPP-63", "HSPP-64", "HSPP-65", "HSPP-66", "HSPP-67", "HSPP-68", "HSPP-69", "HSPP-70", "HSPP-71", "HSPP-72", "HSPP-73", "HSPP-74", "HSPP-75", "HSPP-76", "HSPP-77", "HSPP-78", "HSPP-79", "HSPP-80", "HSPP-81", "HSPP-82", "HSPP-83", "HSPP-84", "HSPP-85", "HSPP-86", "HSPP-87", "HSPP-88", "HSPP-89", "HSPP-90", "HSPP-91", "HSPP-92", "HSPP-93", "HSPP-94", "HSPP-95", "HSPP-96", "HSPP-97", "HSPP-98", "HSPP-99", "HSPP-100", "HSPP-

101", "HSPP-102", "HSPP-103", "HSPP-104", "HSPP-105", "HSPP-106", "HSPP-107",
"HSPP-108", "HSPP-109", "HSPP-110", "HSPP-111", "HSPP-112", "HSPP-113", "HSPP-
114", "HSPP-115", "HSPP-116", "HSPP-117", "HSPP-118", "HSPP-119", "HSPP-120",
"HSPP-121", "HSPP-122", "HSPP-123", "HSPP-124", "HSPP-125", "HSPP-126",
5 "HSPP-127", "HSPP-128", "HSPP-129", "HSPP-130", "HSPP-131", "HSPP-132",
"HSPP-133", and "HSPP-134". In one aspect, the invention provides a substantially
purified polypeptide comprising an amino acid sequence selected from the group
consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5,
SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
10 NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16,
SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ
ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID
NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID
NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37,
15 SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ
ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID
NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53,
SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ
ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID
20 NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69,
SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ
ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID
NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85,
SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ
25 ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID
NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID
NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID
NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID
NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID
30 NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID
NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID

NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134 (SEQ ID NO:1-134), and fragments thereof.

The invention further provides a substantially purified variant having at least 90% amino acid identity to at least one of the amino acid sequences selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID

NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268 (SEQ ID NO:135-268), and fragments thereof. The invention further provides an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide sequence selected from the group consisting of SEQ ID NO:135-268, and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:135-268, and fragments thereof.

The invention also provides a method for detecting a polynucleotide in a sample containing nucleic acids, the method comprising the steps of (a) hybridizing the complement of the polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. In another aspect, the expression vector is contained within a host cell.

The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also provides a purified agonist and a purified antagonist to the polypeptide.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

BRIEF DESCRIPTION OF THE TABLE

Table 1 shows nucleotide and polypeptide sequence identification numbers (SEQ ID NO), clone identification numbers (clone ID), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding HSPP.

Table 2 shows features of each polypeptide sequence, including predicted signal peptide sequences, and methods and algorithms used for identification of HSPP.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis, diseases, disorders, or conditions associated with these tissues, and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which
5 Incyte cDNA clones encoding HSPP were isolated.

Table 5 shows the programs, their descriptions, references, and threshold parameters used to analyze HSPP.

Table 6 shows the regions of the full-length nucleotide sequences of HSPP to which cDNA fragments of Table 1 correspond.

10

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology
15 used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise.
20 Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this
25 invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with
30 the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"HSPP" refers to the amino acid sequences of substantially purified HSPP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural,
5 synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which, when bound to HSPP, increases or prolongs the duration of the effect of HSPP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of HSPP.

An "allelic variant" is an alternative form of the gene encoding HSPP. Allelic
10 variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these
15 types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding HSPP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as HSPP or a polypeptide with at least one functional characteristic of HSPP.
20 Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding HSPP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding HSPP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of
25 amino acid residues which produce a silent change and result in a functionally equivalent HSPP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of HSPP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid,
30 positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine,

isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring
5 or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of HSPP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of HSPP. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule,
10 "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

15 The term "antagonist" refers to a molecule which, when bound to HSPP, decreases the amount or the duration of the effect of the biological or immunological activity of HSPP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of HSPP.

The term "antibody" refers to intact molecules as well as to fragments thereof, such
20 as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind HSPP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be
25 conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a
30 protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete

with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence.

5 Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

10 The term "biologically active," refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic HSPP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

15 The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules.

20 The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" or a "composition
25 comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding HSPP or fragments of HSPP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent
30 such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus sequence” refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW Fragment Assembly system (GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

The term “correlates with expression of a polynucleotide” indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding HSPP, by northern analysis is indicative of the presence of nucleic acids encoding HSPP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding HSPP.

A “deletion” refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term “derivative” refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

The term “similarity” refers to a degree of complementarity. There may be partial similarity or complete similarity. The word “identity” may substitute for the word “similarity.” A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as “substantially similar.” The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require

that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or
5 probe will not hybridize to the second non-complementary target sequence.

The phrases "percent identity" or "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Madison WI) which creates alignments between two or more sequences
10 according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) Gene 73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of
15 sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known
20 in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol. 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the
25 elements required for stable mitotic chromosome segregation and maintenance.

The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to any process by which a strand of nucleic acid binds with
30 a complementary strand through base pairing.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary

bases. A hybridization complex may be formed in solution (e.g., C_{0t} or R_{0t} analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" or "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" or "array element" in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term "modulate" refers to a change in the activity of HSPP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of HSPP.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which, comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:135-268, for example, as distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:135-268 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:135-268 from related polynucleotide sequences. A fragment of SEQ ID NO:135-268 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:135-268 and the region of SEQ ID NO:135-268 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based

on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

The terms "operably associated" or "operably linked" refer to functionally related
5 nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator
10 sequences that control expression of the polypeptide.

The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms
15 "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers
20 solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding HSPP, or fragments thereof, or HSPP itself, may comprise a bodily
25 fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" or "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction
30 is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the

presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of HSPP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g.,

replacement of leucine with isoleucine). More rarely, a variant may have “nonconservative” changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without
5 abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term “variant,” when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to HSPP. This definition may also include, for example, “allelic” (as defined above), “splice,” “species,” or “polymorphic” variants.
10 A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will
15 have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass “single nucleotide polymorphisms” (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state,
20 or a propensity for a disease state.

THE INVENTION

The invention is based on the discovery of new human signal peptide-containing proteins (HSPP), the polynucleotides encoding HSPP, and the use of these compositions
25 for the diagnosis, treatment, or prevention of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders.

Table 1 lists the Incyte Clones used to derive full length nucleotide sequences encoding HSPP. Columns 1 and 2 show the sequence identification numbers (SEQ ID
30 NO) of the amino acid and nucleic acid sequences, respectively. Column 3 shows the Clone ID of the Incyte Clone in which nucleic acids encoding each HSPP were identified, and column 4, the cDNA libraries from which these clones were isolated. Column 5

shows Incyte clones, their corresponding cDNA libraries, and shotgun sequences. The clones and shotgun sequences are part of the consensus nucleotide sequence of each HSPP and are useful as fragments in hybridization technologies.

Table 6 shows the regions of the full-length nucleotide sequences of HSPP to which cDNA fragments of Table 1 correspond. Column 1 lists nucleotide sequence identifiers and column 2 shows the clone ID of the Incyte clone in which nucleic acids encoding each HSPP were identified. Column 3 shows Incyte clones and shotgun sequences which are part of the consensus nucleotide sequence of each HSPP and are useful as fragments in hybridization technologies. Column 4 lists the starting nucleotide position and column 5 the ending nucleotide position of the region of the full-length HSPP to which the cDNA fragment corresponds.

The columns of Table 2 show various properties of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3, potential phosphorylation sites; column 4, potential glycosylation sites; column 5, the amino acid residues comprising signature sequences and motifs; column 6, the identity of each protein; and column 7, analytical methods used to identify each HSPP as a signal peptide-containing protein. Note that in column 5, the first line of each cell lists the amino acid residues comprising predicted signal peptide sequences. Additional identifying motifs or signatures are also listed in column 5. Of particular note is the presence of a glycosyl hydrolase family 9 active site signature in SEQ ID NO:126, a ribosomal protein S18 signature in SEQ ID NO:127, an adrenodoxin family iron-sulfur binding region signature and a cytochrome c family heme-binding site signature in SEQ ID NO:132, and a urotensin II signature sequence in SEQ ID NO:96.

Using BLAST, SEQ ID NO:68 (HSPP-68) has been identified as a TWIK-related acid-sensitive K⁺ channel, and SEQ ID NO:92 (HSPP-92) has been identified as a tyrosine-specific protein phosphatase. The tyrosine-specific protein phosphatases signature in SEQ ID NO:92 (HSPP-92) from about V328 through about F340 (including the putative active site cysteine residue at C330) was identified using BLOCKS and PRINTS. Also of note is the identification of SEQ ID NO:66 (HSPP-66) as a steroid binding protein using BLAST.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding HSPP. The first column of Table 3 lists the nucleotide sequence identifiers. The second column lists tissue categories which express HSPP as a fraction of total tissue categories expressing HSPP. The third column lists the diseases, disorders, or conditions associated with those tissues expressing HSPP. The fourth column lists the vectors used to subclone the cDNA library. Of particular note is the expression of SEQ ID NO:200, SEQ ID NO:203, and SEQ ID NO:225 in lung tissues; the expression of SEQ ID NO:212, SEQ ID NO:216, and SEQ ID NO:220 in reproductive tissues; the expression of SEQ ID NO:223 in cancerous tissues; the expression of SEQ ID NO:232 in gastrointestinal tissue, specifically the small intestine or colon (fifteen out of sixteen (93.8%) cDNA libraries); and the expression of SEQ ID NO:224 in cancerous and proliferating tissues. Also of particular interest is the tissue-specific expression of SEQ ID NO:252 and SEQ ID NO:257. SEQ ID NO:252 is derived from OVARTUT01, an ovarian tumor cDNA library and is exclusively expressed in reproductive tumor tissue. SEQ ID NO:257 is derived from THP1AZT01, a 5-aza-2'-deoxycytidine treated human promonocyte cDNA library and is exclusively expressed in hematopoietic tissue.

The following fragments of the nucleotide sequences encoding HSPP are useful in hybridization or amplification technologies to identify SEQ ID NO:135-268 and to distinguish between SEQ ID NO:135-268 and related polynucleotide sequences. The useful fragments are the fragment of SEQ ID NO:230 from about nucleotide 75 to about nucleotide 104; the fragment of SEQ ID NO:231 from about nucleotide 210 to about nucleotide 239; the fragment of SEQ ID NO:232 from about nucleotide 157 to about nucleotide 186; the fragment of SEQ ID NO:233 from about nucleotide 268 to about nucleotide 297; the fragment of SEQ ID NO:234 from about nucleotide 160 to about nucleotide 186; the fragment of SEQ ID NO:235 from about nucleotide 201 to about nucleotide 230; the fragment of SEQ ID NO:236 from about nucleotide 165 to about nucleotide 194; the fragment of SEQ ID NO:237 from about nucleotide 366 to about nucleotide 395; the fragment of SEQ ID NO:238 from about nucleotide 714 to about nucleotide 743; the fragment of SEQ ID NO:239 from about nucleotide 1731 to about nucleotide 1760; the fragment of SEQ ID NO:240 from about nucleotide 419 to about nucleotide 448; the fragment of SEQ ID NO:241 from about nucleotide 494 to about

nucleotide 523; the fragment of SEQ ID NO:242 from about nucleotide 100 to about nucleotide 129; the fragment of SEQ ID NO:243 from about nucleotide 104 to about nucleotide 133; the fragment of SEQ ID NO:244 from about nucleotide 136 to about nucleotide 165; the fragment of SEQ ID NO:245 from about nucleotide 140 to about
5 nucleotide 169; the fragment of SEQ ID NO:246 from about nucleotide 125 to about nucleotide 154; the fragment of SEQ ID NO:247 from about nucleotide 687 to about nucleotide 758; the fragment of SEQ ID NO:248 from about nucleotide 327 to about nucleotide 398; the fragment of SEQ ID NO:249 from about nucleotide 741 to about nucleotide 785; the fragment of SEQ ID NO:250 from about nucleotide 184 to about
10 nucleotide 255; the fragment of SEQ ID NO:251 from about nucleotide 165 to about nucleotide 242; the fragment of SEQ ID NO:252 from about nucleotide 271 to about nucleotide 342; the fragment of SEQ ID NO:253 from about nucleotide 1081 to about nucleotide 1152; the fragment of SEQ ID NO:254 from about nucleotide 781 to about nucleotide 852; the fragment of SEQ ID NO:255 from about nucleotide 620 to about
15 nucleotide 691; the fragment of SEQ ID NO:256 from about nucleotide 872 to about nucleotide 916; the fragment of SEQ ID NO:257 from about nucleotide 242 to about nucleotide 313; the fragment of SEQ ID NO:258 from about nucleotide 595 to about nucleotide 648; the fragment of SEQ ID NO:259 from about nucleotide 163 to about nucleotide 216; the fragment of SEQ ID NO:260 from about nucleotide 244 to about
20 nucleotide 315; the fragment of SEQ ID NO:261 from about nucleotide 75 to about nucleotide 128; the fragment of SEQ ID NO:262 from about nucleotide 650 to about nucleotide 703; the fragment of SEQ ID NO:263 from about nucleotide 143 to about nucleotide 214; the fragment of SEQ ID NO:264 from about nucleotide 434 to about nucleotide 487; the fragment of SEQ ID NO:265 from about nucleotide 218 to about
25 nucleotide 271; the fragment of SEQ ID NO:266 from about nucleotide 89 to about nucleotide 145; the fragment of SEQ ID NO:267 from about nucleotide 198 to about nucleotide 254; and the fragment of SEQ ID NO:268 from about nucleotide 10 to about nucleotide 54.

The invention also encompasses HSPP variants. A preferred HSPP variant is one
30 which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the HSPP amino acid sequence, and which contains at least one functional or structural characteristic of HSPP.

The invention also encompasses polynucleotides which encode HSPP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:135-268, which encodes HSPP.

5 The invention also encompasses a variant of a polynucleotide sequence encoding HSPP. In particular, such a variant polynucleotide sequence will have at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding HSPP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence
10 selected from the group consisting of SEQ ID NO:135-268 which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:135-268. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of
15 HSPP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding HSPP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible
20 variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring HSPP, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode HSPP and its variants are preferably
25 capable of hybridizing to the nucleotide sequence of the naturally occurring HSPP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding HSPP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or
30 eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding HSPP and its derivatives without altering the encoded amino acid sequences include the

production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode HSPP and HSPP derivatives, or fragments thereof, entirely by synthetic chemistry. After
5 production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding HSPP or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable
10 of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:135-268 and fragments thereof under various conditions of stringency, (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably
15 less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily
20 include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as
25 needed. In a preferred embodiment, hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50
30 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the Hamilton MICROLAB 2200 (Hamilton, Reno NV), Peltier Thermal Cycler 200 (PTC200; MJ Research, Watertown MA) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using either ABI 373 or 377 DNA sequencing systems (Perkin-Elmer) or the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA). The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding HSPP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect

upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses
5 primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome
10 DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-306).
15 Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate
20 program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in
25 which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic
30 separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g.,

GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

5 In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode HSPP may be cloned in recombinant DNA molecules that direct expression of HSPP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be
10 produced and used to express HSPP.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter HSPP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR
15 reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding HSPP may be synthesized, in whole
20 or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.) Alternatively, HSPP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.)
25 Automated synthesis may be achieved using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of HSPP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid
30 chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid

analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active HSPP, the nucleotide sequences encoding HSPP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding HSPP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding HSPP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding HSPP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding HSPP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding HSPP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral

expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding HSPP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding HSPP can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding HSPP into the vector's multiple cloning site disrupts the lacZ gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of HSPP are needed, e.g. for the production of antibodies, vectors which direct high level expression of HSPP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of HSPP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Grant et al. (1987) Methods Enzymol. 153:516-54; and Scorer, C. A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of HSPP. Transcription of sequences encoding HSPP may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated

transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding HSPP
5 may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses HSPP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be
10 used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods
15 (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of HSPP in cell lines is preferred. For example, sequences encoding HSPP can be transformed into cell lines using expression vectors which may contain viral origins of
20 replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the
25 introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *apr* cells, respectively. (See,
30 e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to

the aminoglycosides, neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-3570; Colbère-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*,
5 which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of
10 transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding HSPP is inserted within a marker gene sequence,
15 transformed cells containing sequences encoding HSPP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding HSPP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

20 In general, host cells that contain the nucleic acid sequence encoding HSPP and that express HSPP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or
25 quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of HSPP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site,
30 monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on HSPP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al.

(1990) Serological Methods, a Laboratory Manual, APS Press, St Paul MN, Sect. IV; Coligan, J. E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

5 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding HSPP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding
10 HSPP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia
15 Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding HSPP may be cultured
20 under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode HSPP may be designed to contain signal sequences which direct secretion of HSPP through a prokaryotic
25 or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing
30 which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK,

HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Manassas, VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding HSPP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric HSPP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of HSPP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the HSPP encoding sequence and the heterologous protein sequence, so that HSPP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled HSPP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of HSPP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A Peptide

Synthesizer (Perkin-Elmer). Various fragments of HSPP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

5 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of HSPP and signal peptide sequences. In addition, chemical and structural similarity, in the context of sequences and motifs, exists between HSPP-66 and prostatic steroid-binding C3 precursor from rat (GI 206453); between HSPP-68 and TWIK-related acid-sensitive K⁺channel from human (GI 2465542); and between HSPP-92
10 and tyrosine specific protein phosphatases (PROSITE PDOC00323). In addition, the expression of HSPP is closely associated with proliferative, cancerous, inflamed, cardiovascular, nervous, reproductive, hematopoietic/immune, and developmental tissue. Therefore, HSPP appears to play a role in cell proliferative disorders including cancer; inflammation; and cardiovascular,
15 neurological, reproductive, and developmental disorders. In the treatment of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders associated with increased HSPP expression or activity, it is desirable to decrease the expression or activity of HSPP. In the treatment of the above conditions associated with decreased HSPP expression or activity, it is desirable
20 to increase the expression or activity of HSPP.

Therefore, in one embodiment, HSPP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of HSPP. Examples of such disorders include, but are not limited to, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis,
25 bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia,
30 gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; inflammatory disorders, such as acquired immunodeficiency syndrome (AIDS), Addison's

disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, 5 dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, 10 polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis. Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections. and trauma; cardiovascular disorders including 15 disorders of the blood vessels such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, and vascular tumors; disorders of the heart such as congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve 20 stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, and congenital heart disease; and disorders of the lungs such as congenital lung anomalies, atelectasis, 25 pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse 30 interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary

hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, and pleural tumors; neurological disorders such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; reproductive disorders such as disorders of prolactin production; infertility, including tubal disease, ovulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, carcinoma of the male breast, and gynecomastia; and developmental disorders, such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental

retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss.

In another embodiment, a vector capable of expressing HSPP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of HSPP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified HSPP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of HSPP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of HSPP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of HSPP including, but not limited to, those listed above.

In a further embodiment, an antagonist of HSPP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of HSPP. Examples of such disorders include, but are not limited to, those described above. In one aspect, an antibody which specifically binds HSPP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express HSPP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding HSPP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of HSPP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act

synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of HSPP may be produced using methods which are generally known in the art. In particular, purified HSPP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind HSPP. Antibodies to HSPP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with HSPP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to HSPP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of HSPP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to HSPP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42;

Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule
5 with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce HSPP-specific single chain
10 antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) Proc. Natl. Acad. Sci. 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly
15 specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86: 3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for HSPP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by
20 reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the
25 desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between HSPP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering HSPP
30 epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for HSPP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of HSPP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple HSPP epitopes, represents the average affinity, or avidity, of the antibodies for HSPP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular HSPP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the HSPP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of HSPP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington, DC; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of HSPP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding HSPP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding HSPP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding HSPP. Thus, complementary molecules or fragments may be used to modulate HSPP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and

sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding HSPP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding HSPP. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

Genes encoding HSPP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding HSPP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding HSPP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by

endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding HSPP.

Specific ribozyme cleavage sites within any potential RNA target are initially
5 identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be
10 evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase
15 phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding HSPP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell
20 lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is
25 inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and
30 equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or

by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses,
5 rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of HSPP, antibodies to HSPP, and mimetics, agonists,
10 antagonists, or inhibitors of HSPP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

15 The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may
20 contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

25 Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

30 Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be

added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including
5 arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc,
10 polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules
15 made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with
20 or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such
25 as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain
30 suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of HSPP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example HSPP or fragments thereof, antibodies of HSPP, and agonists, antagonists or inhibitors of HSPP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically

effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about $0.1 \mu\text{g}$ to $100,000 \mu\text{g}$, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

25 DIAGNOSTICS

In another embodiment, antibodies which specifically bind HSPP may be used for the diagnosis of disorders characterized by expression of HSPP, or in assays to monitor patients being treated with HSPP or agonists, antagonists, or inhibitors of HSPP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for HSPP include methods which utilize the antibody and a label to detect HSPP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled

by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring HSPP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of HSPP expression. Normal or standard values for HSPP expression are established by combining
5 body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to HSPP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of HSPP expressed in subject, control, and disease samples
10 from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding HSPP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The
15 polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of HSPP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of HSPP, and to monitor regulation of HSPP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting
20 polynucleotide sequences, including genomic sequences, encoding HSPP or closely related molecules may be used to identify nucleic acid sequences which encode HSPP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will
25 determine whether the probe identifies only naturally occurring sequences encoding HSPP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the HSPP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be
30 derived from the sequence of SEQ ID NO:135-268 or from genomic sequences including promoters, enhancers, and introns of the HSPP gene.

Means for producing specific hybridization probes for DNAs encoding HSPP include the cloning of polynucleotide sequences encoding HSPP or HSPP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding HSPP may be used for the diagnosis of disorders associated with expression of HSPP. Examples of such disorders include, but are not limited to, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; inflammatory disorders, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic,

protozoal, and helminthic infections, and trauma; cardiovascular disorders including disorders of the blood vessels such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, and vascular tumors; disorders of the heart such as congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, and congenital heart disease; and disorders of the lungs such as congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, and pleural tumors; neurological disorders such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal

hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; reproductive disorders such as disorders of prolactin production; infertility, including tubal disease, ovulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, carcinoma of the male breast, and gynecomastia; and developmental disorders, such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss. The polynucleotide sequences encoding HSPP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered HSPP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding HSPP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding HSPP may be labeled by standard methods and added

to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding HSPP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of HSPP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding HSPP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding HSPP may involve the use of PCR. These oligomers may be chemically

synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding HSPP, or a fragment of a polynucleotide complementary to the polynucleotide encoding HSPP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may
5 also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of HSPP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J.
10 Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of
15 the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic
20 agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al.
25 (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding HSPP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a
30 specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries.

(See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. 5 (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding HSPP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention 10 may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another 15 mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to 20 a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

25 In another embodiment of the invention, HSPP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between HSPP and the agent being 30 tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen,

et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with HSPP, or fragments thereof, and washed. Bound HSPP is then detected by methods well known in the art. Purified HSPP can also be coated directly onto plates for use in the
5 aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding HSPP specifically compete with a test compound for binding HSPP. In this manner, antibodies can be used to detect the
10 presence of any peptide which shares one or more antigenic determinants with HSPP.

In additional embodiments, the nucleotide sequences which encode HSPP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair
15 interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

20 The disclosures of all applications, patents, and publications, mentioned above and below, in particular US Ser. No. 60/090,762, US Ser. No. 60/094,983, US Ser. No. 60/102,686, and US Ser. No. 60/112,129, are hereby expressly incorporated by reference.

EXAMPLES

25 I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine
30 isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6). Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision, using the UNIZAP vector system (Stratagene) or cell lysis. Plasmids were purified using at least one of the following: a MAGIC or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the REAL Prep 96 plasmid kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

The cDNAs were prepared for sequencing using the ABI CATALYST 800 (Perkin-Elmer) or the HYDRA microdispenser (Robbins Scientific) or MICROLAB 2200 (Hamilton) systems in combination with the PTC-200 thermal cyclers (MJ Research). The cDNAs were sequenced using the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) and standard ABI protocols, base calling software, and kits. In one alternative, cDNAs were sequenced using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics). In another alternative, the cDNAs were amplified and sequenced using the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer). In yet another alternative, cDNAs were sequenced using solutions and dyes from Amersham Pharmacia Biotech. Reading frames for the ESTs were determined using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA, extension, and shotgun sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the software programs, descriptions, references, and threshold parameters used. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides a brief description thereof, the third column presents the references which are incorporated by reference herein, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the probability the greater the homology). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based

on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation, using programs based on BLAST, FASTA, and BLIMPS. The sequences were
5 assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the
10 GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) Cur. Opin. Str. Biol. 6:361-365.)

The programs described above for the assembly and analysis of full length
15 polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:135-268. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

20 Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical
25 or related molecules in nucleotide databases such as GenBank or LIFESEQ database (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

30
$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

100

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product
5 scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding HSPP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal,
10 hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific
15 expression are reported in Table 3.

V. Extension of HSPP Encoding Polynucleotides

Full length nucleic acid sequences of SEQ ID NOs:135-229 were produced by extension of the component fragments described in Table 1, column 5, using oligonucleotide primers based on these fragments. For each nucleic acid sequence, one
20 primer was synthesized to initiate extension of an antisense polynucleotide, and the other was synthesized to initiate extension of a sense polynucleotide. Primers were used to facilitate the extension of the known sequence "outward" generating amplicons containing new unknown nucleotide sequence for the region of interest. The initial primers were designed from the cDNA using OLIGO™ 4.06 (National Biosciences, Plymouth, MN), or
25 another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries (GIBCO BRL) were used to extend the sequence.
30 If more than one extension is necessary or desired, additional sets of primers are designed to further extend the known region.

High fidelity amplification was obtained by following the instructions for the XL-PCR™ kit (The Perkin-Elmer Corp., Norwalk, CT) and thoroughly mixing the enzyme and reaction mix. PCR was performed using the PTC-200 thermal cycler (MJ Research, Inc., Watertown, MA), beginning with 40 pmol of each primer and the recommended

5 concentrations of all other components of the kit, with the following parameters:

	Step 1	94° C for 1 min (initial denaturation)
	Step 2	65° C for 1 min
	Step 3	68° C for 6 min
	Step 4	94° C for 15 sec
10	Step 5	65° C for 1 min
	Step 6	68° C for 7 min
	Step 7	Repeat steps 4 through 6 for an additional 15 cycles
	Step 8	94° C for 15 sec
	Step 9	65° C for 1 min
15	Step 10	68° C for 7:15 min
	Step 11	Repeat steps 8 through 10 for an additional 12 cycles
	Step 12	72° C for 8 min
	Step 13	4° C (and holding)

20 A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6% to 0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were excised from the gel, purified using QIAQUICK™ (QIAGEN Inc.), and trimmed of overhangs using Klenow enzyme to facilitate religation and cloning.

25 After ethanol precipitation, the products were redissolved in 13 μ l of ligation buffer, 1 μ l T4-DNA ligase (15 units) and 1 μ l T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2 to 3 hours, or overnight at 16° C. Competent *E. coli* cells (in 40 μ l of appropriate media) were transformed with 3 μ l of ligation mixture and cultured in 80 μ l of SOC medium. (See, e.g., Sambrook, *supra*,
 30 Appendix A, p. 2.) After incubation for one hour at 37° C, the *E. coli* mixture was plated on Luria Bertani (LB) agar (See, e.g., Sambrook, *supra*, Appendix A, p. 1) containing carbenicillin (2x carb). The following day, several colonies were randomly picked from each plate and cultured in 150 μ l of liquid LB/2x carb medium placed in an individual well of an appropriate commercially-available sterile 96-well microtiter plate. The
 35 following day, 5 μ l of each overnight culture was transferred into a non-sterile 96-well plate and, after dilution 1:10 with water, 5 μ l from each sample was transferred into a PCR array.

For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer, and one or both of the gene specific primers used for the extension reaction were added to each well. Amplification was performed using the following conditions:

5	Step 1	94° C for 60 sec
	Step 2	94° C for 20 sec
	Step 3	55° C for 30 sec
	Step 4	72° C for 90 sec
	Step 5	Repeat steps 2 through 4 for an additional 29 cycles
10	Step 6	72° C for 180 sec
	Step 7	4° C (and holding)

Aliquots of the PCR reactions were run on agarose gels together with molecular weight markers. The sizes of the PCR products were compared to the original partial
15 cDNAs, and appropriate clones were selected, ligated into plasmid, and sequenced.

The full length nucleic acid sequences of SEQ ID NO:230-268 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known
20 fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

25 Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer,
30 reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7:
35 storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as

follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl
5 PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl
10 aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham
15 Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into
20 competent E. coli cells. Transformed cells were selected on antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with
25 the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulphoxide (1:2,
30 v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

In like manner, the nucleotide sequences of SEQ ID NO:135-268 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

5 VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:135-268 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT-AR film (Eastman Kodak, Rochester NY) is exposed to the blots to film for several hours, hybridization patterns are compared visually.

25 VII. Microarrays

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, *supra*.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of

complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

VIII. Complementary Polynucleotides

Sequences complementary to the HSPP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring HSPP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of HSPP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the HSPP-encoding transcript.

IX. Expression of HSPP

Expression and purification of HSPP is achieved using bacterial or virus-based expression systems. For expression of HSPP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria

express HSPP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG).

Expression of HSPP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding HSPP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, HSPP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from HSPP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified HSPP obtained by these methods can be used directly in the following activity assay.

25

X. Demonstration of HSPP Activity

HSPP-68

HSPP-68 activity is measured by determining the potassium current using voltage clamp analysis on single Xenopus laevis oocytes injected with HSPP-68 cRNA. HSPP-68 cRNA is synthesized in vitro from linearized HSPP-68 encoding plasmids using the T7

RNA polymerase and injected into oocytes.. Injected oocytes are used two to four days after injection. In a 0.3 ml perfusion chamber, a single oocyte is impaled with two standard microelectrodes (1-2.5 M Ω) filled with 3 M KCl. The oocyte is maintained under voltage clamp by using a Dagan TEV 200 amplifier, in buffer containing 96 mM NaCl, 2 mM KCl, 1.8 mM CaCl₂, 2 mM MgCl₂, 5 mM HEPES, pH 7.4 with NaOH. Stimulation of the preparation, data acquisition, and analysis is performed using a computer. All experiments are performed at room temperature (21-22 °C). Following a depolarizing pulse, the characteristics of the resulting potassium current are measured via the recording electrode. The amount of potassium current that flows in response to a unit depolarization is proportional to the activity of HSPP-68 in the cell. (Duprat, F. et al. (1997) EMBO J. 16:5464-5471.)

HSPP-92

HSPP-92 protein phosphatase activity is measured by the hydrolysis of P-nitrophenyl phosphate (PNPP). HSPP-92 is incubated together with PNPP in HEPES buffer pH 7.5, in the presence of 0.1% b-mercaptoethanol at 37°C for 60 min. The reaction is stopped by the addition of 6 ml of 10 N NaOH and the increase in light absorbance at 410 nm resulting from the hydrolysis of PNPP is measured using a spectrophotometer. The increase in light absorbance is proportional to the activity of PP in the assay. (Diamond R.H. et al (1994) Mol Cell Biol 14:3752-62.)

Alternatively, HSPP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled HSPP, washed, and any wells with labeled HSPP complex are assayed. Data obtained using different concentrations of HSPP are used to calculate values for the number, affinity, and association of HSPP with the candidate molecules.

Alternatively, an assay for HSPP activity measures the expression of HSPP on the cell surface. cDNA encoding HSPP is subcloned into an appropriate mammalian expression vector suitable for high levels of cDNA expression. The resulting construct is transfected into a nonhuman cell line such as NIH3T3. Cell surface proteins are labeled with biotin using methods known in the art. Immunoprecipitations are performed using HSPP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to

unlabeled immunoprecipitant is proportional to the amount of HSPP expressed on the cell surface.

Alternatively, an assay for HSPP activity measures the amount of HSPP in secretory, membrane-bound organelles. Transfected cells as described above are harvested and lysed. The lysate is fractionated using methods known to those of skill in the art, for example, sucrose gradient ultracentrifugation. Such methods allow the isolation of subcellular components such as the Golgi apparatus, ER, small membrane-bound vesicles, and other secretory organelles. Immunoprecipitations from fractionated and total cell lysates are performed using HSPP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of HSPP in secretory organelles relative to HSPP in total cell lysate is proportional to the amount of HSPP in transit through the secretory pathway.

XI. Functional Assays

HSPP function is assessed by expressing the sequences encoding HSPP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP, and to evaluate properties, for example, their apoptotic state. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in

expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York
5 NY.

The influence of HSPP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding HSPP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently
10 separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding HSPP and other genes of interest can be analyzed by northern analysis or microarray techniques.

15 XII. Production of HSPP Specific Antibodies

HSPP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

20 Alternatively, the HSPP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel,
25 1995, supra, ch. 11.)

Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A Peptide Synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are
30 immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide activity by, for example, binding the peptide to plastic,

blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring HSPP Using Specific Antibodies

Naturally occurring or recombinant HSPP is substantially purified by
5 immunoaffinity chromatography using antibodies specific for HSPP. An immunoaffinity column is constructed by covalently coupling anti-HSPP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

10 Media containing HSPP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of HSPP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/HSPP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and HSPP is collected.

15 XIV. Identification of Molecules Which Interact with HSPP

HSPP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled HSPP, washed, and any wells with labeled HSPP complex are assayed. Data
20 obtained using different concentrations of HSPP are used to calculate values for the number, affinity, and association of HSPP with the candidate molecules.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with
25 specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	135	443531	MPHGNOT03	443531H1 (MPHGNOT03), 1406807F6 (LA TRTUT02), 443531T6 (MPHGNOT03), SBAA00451F1, SBAA00676F1
2	136	632860	NEUTGMT01	632860H1 (NEUTGMT01), 784715R3 (PROSNOT05), 509590H1 (MPHGNOT03)
3	137	670010	CRBLNOT01	670010H1 (CRBLNOT01), 669971R1 (CRBLNOT01), 1553045F1 (BLADTUT04)
4	138	726498	SYNOOA T01	726498H1 (SYNOOA T01), 726498R6 (SYNOOA T01), 866599R3 (BRAITUT03)
5	139	795064	OVARNOT03	795064H1 (OVARNOT03), 4339458H1 (BRAUNOT02), 937605R3 (CERVNOT01), 2381151F6 (ISLTNOT01), 1466346F6 (PANCNOT02)
6	140	924925	BRAINOT04	924925H1 (BRAINOT04), 3268330H1 (BRAINOT20), 759120R3 (BRAITUT02)
7	141	962390	BRSTTUT03	962390H1 (BRSTTUT03), 1907958F6 (CONNTUT01), 023569F1 (ADENINB01), 167282F1 (LIVRNOT01), 1309211F1 (COLNFET02), SAUA00696F1, SAUA02860F1
8	142	1259405	MENITUT03	1259405H1 (MENITUT03), 2472425H1 (THPINOT03), 774303R1 (COLNNOT05), 1520779F1 (BLADTUT04), 1693833F6 (COLNNOT23), 1831858T6.comp (THPIAZT01), 1527737T6.comp (UCMCL5T01)
9	143	1297384	BRSTNOT07	1297384H1 (BRSTNOT07), 1269310F6 (BRAINOT09), 1457367F1 (COLNFET02), 415587R1 (BRSTNOT01), SANA02967F1
10	144	1299627	BRSTNOT07	1299627H1 (BRSTNOT07), 1359140F6 (LUNGNOT09), 1349224F1 (LA TRTUT02), SBAA01431F1, SBAA02909F1, SBAA01156F1
11	145	1306026	PLACNOT02	1306026H1 (PLACNOT02), 1464088R6 (PANCNOT04), SBAA02496F1, SBAA04305F1
12	146	1316219	BLADTUT02	1316219H1 (BLADTUT02), 2458603F6 (ENDANOT01), 2504756T6 (CONUTUT01)
13	147	1329031	PANCNOT07	1329031H1 (PANCNOT07), 1329031T6 (PANCNOT07), 1329031F6 (PANCNOT07)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
14	148	1483050	CORPNOT02	1483050HI (CORPNOT02), 855049HI (NGANNT01), 077017FI (SYNORAB01), 1483050F6 (CORPNOT02), 1480024T6 (CORPNOT02), 1483050T6 (CORPNOT02), 759486RI (BRAITUT02)
15	149	1514160	PANCTUT01	1514160HI (PANCTUT01), 1866765T7 (SKINBIT01), 782676RI (MYOMNOT01), 008055X4 (HMCINOT01), 008055X5 (HMCINOT01), 1866765F6 (SKINBIT01), SAOA03127FI
16	150	1603403	LUNGNOT15	1603403HI (LUNGNOT15), 372910FI (LUNGNOT02), 733299R7 (LUNGNOT03)
17	151	1652303	PROSTUT08	1652303HI (PROSTUT08), 1671806HI (BLADNOT05), 1341743TI (COLNLTUT03), 3803812HI (BLADTUT03), 1878546F6 (LEUKNOT03), 1428640FI (SINTBST01), 2058609R6 (OVARNOT03), 1331621FI (PANCNOT07), 1306331TI (PLACNOT02)
18	152	1693358	COLNNOT23	1693358HI (COLNNOT23), 2498265HI (ADRETUT05), 1867125F6 (SKINBIT01), 1693358T6 (COLNNOT23), 2245848R6 (HIPONON02)
19	153	1707711	DUODNOT02	1707711HI (DUODNOT02), 1484609TI (CORPNOT02), 1707711F6 (DUODNOT02), 1267959FI (BRAINOT09), 1484609FI (CORPNOT02), SAJA00930FI, SAJA01300RI, SAJA00999RI
20	154	1738735	COLNNOT22	1738735HI (COLNNOT22), SAJA00944RI, SAJA00137FI, SAJA03629FI
21	155	1749147	STOMTUT02	1749147HI (STOMTUT02), 1749147F6 (STOMTUT02), 1749147T6 (STOMTUT02)
22	156	1817722	PROSNOT20	1817722HI (PROSNOT20), 2011085HI (TESTNOT03)
23	157	1831290	THP1AZT01	1831290HI (THP1AZT01), 3473958HI (LUNGNOT27), 1972268F6 (UCMCL5T01), 1301277FI (BRSTNOT07), 1521574FI (BLADTUT04), 1561690T6 (SPLNNOT04), 891461RI (STOMTUT01)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
24	158	1831477	THP1AZT01	1831477HI (THP1AZT01), 1582867HI (DUODNOT01), 1336769TI (COLNNOT13), 1933092HI (COLNNOT16), 1519909FI (BLADTUT04), 120946HI (NEUTGMT01), 809556TI (LUNGNOT04), 1217559TI (NEUTGMT01), 1309225FI (COLNFET02)
25	159	1841607	COLNNOT07	1841607HI (COLNNOT07), SBHA03588FI
26	160	1852391	LUNGFET03	1852391HI (LUNGFET03), 734140HI (TONSNOT01), 1852391F6 (LUNGFET03)
27	161	1854555	HNT3AZT01	1854555HI (HNT3AZT01), 2511711HI (CONUTUT01), 782453RI (MYOMNOT01), 1854555F6 (HNT3AZT01), 1840675T6 (COLNNOT07), 2109736HI (BRAITUT03)
28	162	1855755	PROSNOT18	1855755HI (PROSNOT18), 3040236HI (BRSTNOT16), 1283207FI (COLNNOT16), 833763TI (PROSNOT07), 1920926R6 (BRSTTUT01)
29	163	1861434	PROSNOT19	1861434HI (PROSNOT19), 980291RI (TONGTUT01), 1861434T6 (PROSNOT19), SARA01525FI, SARA02548FI
30	164	1872334	LEUKNOT02	1872334HI (LEUKNOT02), 1872334F6 (LEUKNOT02), SBGA03684FI
31	165	1877230	LEUKNOT03	1877230HI (LEUKNOT03), 2519841HI (BRAITUT21), 1877230T6 (LEUKNOT03), 1254693FI (LUNGFET03), 077020RI (SYNORAB01), 1232336FI (LUNGFET03), 1004952R6 (BRSTNOT03), SARA01879FI, SARA02654FI
32	166	1877885	LEUKNOT03	1877885HI (LEUKNOT03), 508020FI (TMLR3DT01), 2751126R6 (THP1AZS08), SARA02571FI
33	167	1889269	BLADTUT07	1889269HI (BLADTUT07), 1915551HI (PROSTUT04), 629493X12 (KIDNNOT05), 1411289FI (THYRNUT03), 1215274X34FI (BRSTTUT01), 1818447F6 (PROSNOT20), 1208463RI (BRSTNOT02)
34	168	1890243	BLADTUT07	1890243HI (BLADTUT07), SARA01884FI, SARA00046FI, SARA03294FI, SARA02790FI

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
35	169	1900433	BLADTUT06	1900433HI (BLADTUT06), SATA00396F1, SATA02742F1
36	170	1909441	CONNTUT01	1909441HI (CONNTUT01), 1398811F1 (BRAITUT08), 3039939HI (BRSTNOT16), 3324740HI (PTHYNOT03), 1442131F6 (THYRNOT03), 2254056HI (OVARUTUT01), 2199453T6 (SPLNFET02), 1692610F6 (COLNNOT23), 1698531HI (BLADTUT05)
37	171	1932226	COLNNOT16	1932226HI (COLNNOT16), 2320569HI (OVARNOT02), 1932226F6 (COLNNOT16), 2469455T6 (THPINOT03), 2469455F6 (THPINOT03), 1907140F6 (OVARNOT07), SATA02592F1
38	172	1932647	COLNNOT16	1932647HI (COLNNOT16), 1492745T1 (PROSNON01), 1492745HI (PROSNON01), SASA02355F1, SASA00117F1, SASA00192F1
39	173	2124245	BRSTNOT07	2124245HI (BRSTNOT07), 1235393F1 (LUNGFET03), 1402264F6 (LATRTUT02), 1303990F1 (PLACNOT02), 1402264T6 (LATRTUT02)
40	174	2132626	OVARNOT03	2132626HI (OVARNOT03), 1723432T6 (BLADNOT06), 2132626R6 (OVARNOT03), 1736723T6 (COLNNOT22), 1504738F1 (BRAITUT07)
41	175	2280639	PROSNON01	2280639HI (PROSNON01), 1435330HI (PANCNOT08), 1377560F6 (LUNGNOT10)
42	176	2292356	BRAINON01	2292356HI (BRAINON01), 4086827HI (LIVRNOT06), 1754442F6 (LIVRTUT01), 3571126HI (HEAPNOT01), 1601305F6 (BLADNOT03)
43	177	2349310	COLSUCT01	2349310HI (COLSUCT01), 2349310T6 (COLSUCT01)
44	178	2373227	ADRENOT07	2373227HI (ADRENOT07), 3316444HI (PROSBPT03), 302685R6 (TESTNOT04), SASA02181F1, SASA01923F1, SASA03516F1
45	179	2457682	ENDANOT01	2457682HI (ENDANOT01), 2457682F6 (ENDANOT01)
46	180	2480426	SMCANOT01	2480426HI (SMCANOT01), 2480426F6 (SMCANOT01)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
47	181	2503743	CONUTUT01	2503743HI (CONUTUT01), 1853909HI (HNT3AZT01), 1517619FI (PANCTUT01), 1467896F6 (PANCTUT02), 490031FI (HNT2AGT01), 1208654RI (BRSTNOT02), 880544RI (THYRN0T02)
48	182	2537684	BONRTUT01	2537684HI (BONRTUT01), 2005493HI (TESTNOT03), 730969HI (LUNGNOT03), 2537601F6 (BONRTUT01), 916487HI (BRSTNOT04), 996135RI (KIDNTUT01), 1920738R6 (BRSTTUT01), 1957710F6 (CONNNOT01)
49	183	2593853	OVARTUT02	2593853HI (OVARTUT02), 807497HI (STOMNOT02), 914020R6 (STOMNOT02), 889992RI (STOMTUT01)
50	184	2622354	KERANOT02	2622354HI (KERANOT02), 2623992HI (KERANOT02), 1556510F6 (BLADTUT04)
51	185	2641377	LUNGTUT08	2641377HI (LUNGTUT08), 4341415H2 (BRAUNOT02), SBDA07049F3
52	186	2674857	KIDNNOT19	2674857HI (KIDNNOT19), 1872373HI (LEUKNOT02), 470512R6 (MMLRIDT01), 1728547HI (PROSNOT14), 3013651F6 (MUSCNOT07), SBDA01366FI, SBDA00694FI
53	187	2758485	THP1AZS08	2758485HI (THP1AZS08), 3097533HI (CERVNOT03), 1578959F6 (DUODNOT01)
54	188	2763296	BRSTNOT12	2763296HI (BRSTNOT12), 3486025F6 (KIDNNOT31), SBDA07002F3
55	189	2779436	OVARTUT03	2779436HI (OVARTUT03), 2779436F6 (OVARTUT03), SBDA07009F3
56	190	2808528	BLADTUT08	2808528HI (BLADTUT08), 2611513F6 (THYMN0T04), SBDA07021T3
57	191	2809230	BLADTUT08	2809230HI (BLADTUT08), 2213849HI (SINTFET03), 711706R6 (SYNORAT04), 958323RI (KIDNNOT05), 030732FI (THPINOB01)
58	192	2816821	BRSTNOT14	2816821HI (BRSTNOT14), 3746964HI (THYMN0T08), 2816821F6 (BRSTNOT14), 948722T6 (PANCN0T05), 807947R6 (STOMNOT02)

TABLE I (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
59	193	2817268	BRSTNOT14	2817268HI (BRSTNOT14), 3591308HI (293TF5T01), 419522RI (BRSTNOT01), 2073028F6 (ISLTNOT01), 1308781F6 (COLNFET02)
60	194	2923165	SININOT04	2923165HI (SININOT04), 2011630HI (TESTNOT03), 1457250F1 (COLNFET02), 754668RI (BRAITUT02), 1406510F6 (LATRTUT02)
61	195	2949822	KIDNFET01	2949822HI (KIDNFET01), SBDA07078F3
62	196	2992192	KIDNFET02	2992192HI (KIDNFET02), 2534324H2 (BRAINOT18), 2815255T6 (OVARNOT10), 1551107T6 (PROSNOT06), 1551107R6 (PROSNOT06)
63	197	2992458	KIDNFET02	2992458HI (KIDNFET02), 2618951HI (GBLANOT01), 1479252F1 (CORPNOT02), 1879054HI (LEUKNOT03), 1879054F6 (LEUKNOT03), 2215240HI (SINTFET03), 1535968T1 (SPLNNOT04)
64	198	3044710	HEAANOT01	3044710HI (HEAANOT01), 3741773HI (MENTNOT01), 859906X42C1 (BRAITUT03), 1534347F1 (SPLNNOT04), 1421122F1 (KIDNNOT09), 1303865F1 (PLACNOT02), 1704452F6 (DUODNOT02), 1251642F1 (LUNGFET03), 1781694R6 (PGANNON02)
65	199	3120415	LUNGTUT13	3120415HI (LUNGTUT13), 1360123T1 (LUNGNOT12), 1375015HI (LUNGNOT10)
66	200	126758	LUNGNOT01	126758HI (LUNGNOT01), 126758X11 (LUNGNOT01), 811864T1 (LUNGNOT04)
67	201	674760	CRBLNOT01	674760HI (CRBLNOT01), 3253976HI (OVRTUN01), SAUA03387F1
68	202	1229438	BRAITUT01	1229438HI (BRAITUT01), 1230616HI (BRAITUT01), 1461187RI (PANCNOT04), 2493039HI (ADRETUT05), 2891628HI (LUNGFET04)
69	203	1236935	LUNGFET03	1236935HI (LUNGFET03), SBAA00983F1, SBAA02057F1, SBAA00170F1
70	204	1359283	LUNGNOT12	1359283HI (LUNGNOT12), SBAA01213F1, SBAA03934F1
71	205	1450703	PENITUT01	551298F1 (BEPINOT01), 551298RI (BEPINOT01), 1450703HI (PENITUT01), 2748715HI (LUNGTUT11)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
72	206	1910668	CONNTUT01	1269346H1 (BRAINO09), 1380872F1 (BRAITUT08), 1910668F6 (CONNTUT01), 1910668H1 (CONNTUT01), SATA02800F1, SATA03799F1, SARA02035F1
73	207	1955143	CONNNOT01	1955143F6 (CONNNOT01), 1955143H1 (CONNNOT01)
74	208	1961637	BRSTNOT04	867025H1 (BRAITUT03), 1961637H1 (BRSTNOT04), 2809064T6 (BLADTUT08), 2938714H1 (THYMFET02), 2956402H1 (KIDNFET01), 3808735T6 (CONTTUT01)
75	209	1990762	CORPNOT02	1990762H1 (CORPNOT02), 1990762T3 (CORPNOT02), SBGA04911F1, SBGA01201F1, SBGA02205F1
76	210	1994131	CORPNOT02	1994131H1 (CORPNOT02), 2645984F6 (OVARUTUT04)
77	211	1997745	BRSTTUT03	1752307F6 (LIVRTUT01), 1853730H1 (HNT3AZT01), 1997745H1 (BRSTTUT03), SAZA00953F1
78	212	2009035	TESTNOT03	2009035H1 (TESTNOT03), 2009035R6 (TESTNOT03)
79	213	2009152	TESTNOT03	2009152H1 (TESTNOT03), 2009152R6 (TESTNOT03), 2783263H1 (BRSTNOT13)
80	214	2061752	OVARNOT03	2061752H1 (OVARNOT03), 2061752T6 (OVARNOT03), 2732805H1 (OVARUTUT04), SAZA01310F1, SAZA00830F1
81	215	2061933	OVARNOT03	046580R1 (CORNNOT01), 746061R1 (BRAITUT01), 826996R1 (PROSNOT06), 2061933H1 (OVARNOT03)
82	216	2081422	UTRSNOT08	2081422F6 (UTRSNOT08), 2081422H1 (UTRSNOT08), SBGA04793F1, SBGA05657F1, SBDA00065F1
83	217	2101278	BRAITUT02	2101278H1 (BRAITUT02), SAXA00399F1, SAXA01284F1, SAXA01227F1
84	218	2121353	BRSTNOT07	341437H1 (NEUTFM01), 687136H1 (UTRSNOT02), 2121353H1 (BRSTNOT07), SASA01311F1

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
85	219	2241736	PANCTUT02	833263HI (PROSTUT04), 2241736HI (PANCTUT02), SAZA01148F1, SASA03299F1, SASA01349F1
86	220	2271935	PROSNON01	2271935HI (PROSNON01), 2276774HI (PROSNON01), 2760171T6 (THPIAZS08)
87	221	2295344	BRSTNOT05	2295344HI (BRSTNOT05), 3288561F6 (BONRFET01), SBGA01801F1
88	222	2303994	BRSTNOT05	905482T1 (COLNNOT08), 1858636F6 (PROSNOT18), 2303994HI (BRSTNOT05)
89	223	2497805	ADRETUT05	2497805F6 (ADRETUT05), 2497805HI (ADRETUT05)
90	224	2646362	LUNGTUT11	1754702HI (LIVRTUT01), 2640776T6 (LUNGTUT08), 2646362HI (LUNGTUT11), 3356773HI (PROSTUT16)
91	225	2657146	LUNGTUT09	2657146F6 (LUNGTUT09), 2657146HI (LUNGTUT09)
92	226	2755786	THPIAZS08	288436R1 (EOSIHET02), 1252824F6 (LUNGFET03), 1305549HI (PLACNOT02), 1364975R1 (SCORNON02), 2018293HI (THPINOT01), 2047320HI (THPI77T01), 2184537F6 (SININOT01), 2755786HI (THPIAZS08), 4111022HI (PROSBPT07)
93	227	2831245	TLYMNOT03	2831245HI (TLYMNOT03), SBMA01396F1
94	228	3116250	LUNGTUT13	126263F1 (LUNGNOT01), 2729942HI (OVRTUT04), 3116250HI (LUNGTUT13)
95	229	3129630	LUNGTUT12	3129630F6 (LUNGTUT12), 3129630HI (LUNGTUT12), SBDA06436F1
96	230	007632	HMCINOT01	007632HI (HMCINOT01), 007632R6 (HMCINOT01), 007632T6 (HMCINOT01)
97	231	1236968	LUNGFET03	1236968HI (LUNGFET03), SBAA02713F1, SBAA03203F1, SBAA04196F1
98	232	1334153	COLNNOT13	776410R1 (COLNNOT05), 1334153HI (COLNNOT13), 1334153T1 (COLNNOT13), 1800085F6 (COLNNOT27), 2701948HI (OVRTUT10)

TABLE I (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
99	233	1396975	BRAITUT08	864113HI (BRAITUT03), 876139RI (LUNGAST01), 1268313FI (BRAINOT09), 1351348TI (LATRTUT02), 1396975HI (BRAITUT08), 1485768F6 (CORPNOT02), 1815364F6 (PROSNOT20)
100	234	1501749	SINTBST01	079080RI (SYNORAB01), 1501749HI (SINTBST01), 1724970HI (PROSNOT14)
101	235	1575240	LNODNOT03	081858RI (SYNORAB01), 1575240HI (LNODNOT03), 3451462R6 (UTRSNON03)
102	236	1647884	PROSTUT09	1647884HI (PROSTUT09), 1647884T6 (PROSTUT09), 3998922R6 (HNT2AZS07)
103	237	1661144	BRSTNOT09	720941X17 (SYNOOAT01), 1661144HI (BRSTNOT09), 2181782HI (SININOT01)
104	238	1685409	PROSNOT15	755203RI (BRAITUT02), 1226185TI (COLNNOT01), 1300837FI (BRSTNOT07), 1685409HI (PROSNOT15), 1705256HI (DUODNOT02)
105	239	1731419	BRSTTUT08	1731419HI (BRSTTUT08), 1731419X319T3 (BRSTTUT08), 1731419X322FI (BRSTTUT08), 1731419X326FI (BRSTTUT08), 1731419X329FI (BRSTTUT08), 1733786F6 (BRSTTUT08), SZAH01494FI
106	240	2650265	BRSTNOT14	1680316T6 (STOMFET01), 2650265HI (BRSTNOT14), 2650265T6 (BRSTNOT14), 2760588R6 (BRAINOS12)
107	241	2677129	KIDNNOT19	1592129HI (CARGNOT01), 2645962HI (OVARUT04), 2677129F6 (KIDNNOT19), 2677129HI (KIDNNOT19), 2910973HI (KIDNTUT15), 4571722HI (PROSTMT02), 4906791H2 (TLYMNOT08)
108	242	3151073	ADRENON04	3150857T6 (ADRENON04), 3151073HI (ADRENON04), 3151073R6 (ADRENON04)
109	243	3170095	BRSTNOT18	3170095F6 (BRSTNOT18), 3170095HI (BRSTNOT18)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
110	244	3475168	LUNGNOT27	079680F1 (SYNORAB01), 443811T6 (MPHGNOT03), 1509356T6 (LUNGNOT14), 1873596F6 (LEUKNOT02), 2440867H1 (EOSITXT01), 3475168H1 (LUNGNOT27)
111	245	3836893	DENDTNT01	446637H1 (MPHGNOT03), 1219376R6 (NEUTGMT01), 3735467F6 (SMCCNOS01), 3735467T6 (SMCCNOS01), 3836893H1 (DENDTNT01)
112	246	4072159	KIDNNOT26	2129415T6 (KIDNNOT05), 4072159F6 (KIDNNOT26), 4072159H1 (KIDNNOT26)
113	247	1003916	BRSTNOT03	620937R6 (PGANNOT01), 1003916H1 and 1003916R6 (BRSTNOT03), 1413623H1 (BRAINOT12), 1435945F1 (PANCNOT08), 1479127F1 (CORPNOT02), 1969146R6 (BRSTNOT04), 2517587F6 (BRAITUT21), 2967848H1 (SCORNOT04)
114	248	2093492	PANCNOT04	489651H1 (HNT2AGT01), 1265353T1 (SYNORAT05), 1431505R6 (BEPINON01), 1605237F6 (LUNGNOT15), 2093492H1 and 2093492T6 (PANCNOT04), 4195560H1 (COLITUT02)
115	249	2108789	BRAITUT03	2108789H1 and 2108789R6 (BRAITUT03), 2182008T6 (SININOT01), 3255751R6 and 3255751T6 (OVRTUT01)
116	250	2171401	ENDCNOT03	037241F1 (HUVENOB01), 1821492F6 (GBLATUT01), 2055814T6 (BEPINOT01), 2171401F6 and 2171401H1 (ENDCNOT03), 2668952F6 (ESOGTUT02), 3140313H1 and 3140313T6 (SMCCNOT02), 5031775H1 (EPIBTXT01)
117	251	2212530	SINTFET03	187596R6 and 187596T6 (CARDNOT01), 919634R6 (RATRNOT02), 1992331H1 (CORPNOT02), 2062034H1 (OVARNOT03), 2212530F6 and 2212530H1 (SINTFET03), 2520479H1 (BRAITUT21), 2878284F6 (THYRNOT10), 2992354H1 (KIDNFET02), 4020719F6 (BRAXNOT02)
118	252	2253036	OVRTUT01	2253036H1 and 2253036R6 (OVRTUT01)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
119	253	2280161	PROSNON01	482326H1 (HNT2RAT01), 934345H1 (CERVNOT01), 1379358F1 and 1379358T1 (LUNGNOT10), 1438562T1 (PANCNOT08), 1467511F6 (PANCNOT02), 1568138F1 (UTRSNOT05), 1636106T6 (UTRSNOT06), 2134534F6 (ENDCNOT01), 2280161H1 and 2280161X19F1 (PROSNON01), 2789845F6 (COLNTUT16), 3096938H1 (CERVNOT03), 3774621F6 (BRSTNOT25), 422971H1 (PANCNOT07), 5111983H1 (ENDITXT01), 5324177H1 (FIBPFEN06)
120	254	2287485	BRAINON01	1454588F1 (PENITUT01), 1593332F6 (BRAINOT14), 2287485H1 and 2287485R6 (BRAINON01), 3765992H1 (BRSTNOT24), 4374293H1 (CONFNOT03), 4937931H1 (PROSTUS18), SBCA01722F1
121	255	2380344	ISLTNOT01	2380344F6 and 2380344H1 (ISLTNOT01), 2888536T3 (LUNGFET04), SASA03644F1, SASA03689F1
122	256	2383171	ISLTNOT01	956296R1 (KIDNNOT05), 1342250F1 (COLNTUT03), 1468046F1 and 1468046T1 (PANCNOT02), 2383171H1 (ISLTNOT01), SBYA05452U1, SBYA01369U1
123	257	2396046	THPIAZT01	2396046F6, 2396046H1 and 2396118T6 (THPIAZT01)
124	258	2456587	ENDANOT01	2456587H1 and 2456587T6 (ENDANOT01), 2872569H1 (THYRNOT10), SBCA03778F1, SBDA00115F1, SBCA02401F1, SBCA03351F1, SBCA05164F1, SBCA04783F1, SBCA00155F1, SBCA04141F1
125	259	2484813	BONRTUT01	1234970T1 (LUNGFET03), 1338090F6 (COLNNOT13), 2484813H1 (BONRTUT01), SBCA00053F1, SBCA02064F1, SBCA02151F1, SBCA03770F1, SBCA04866F1, SBCA03406F1
126	260	2493851	ADRETUT05	2493851H1 (ADRETUT05), 3805916F6 (BLADTUT03), 4500439H1 and 4500748H1 (BRAVXT02), 5120601H1 (SMCBUNT01)
127	261	2495719	ADRETUT05	603447R1 (BRSTTUT01), 2495719H1 (ADRETUT05), 2917493F6 (THYMFET03), 4647103H1 (PROSTUT20), SBRA04984D1

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
128	262	2614153	GBLANOT01	1833135R6 (BRAINON01), 1966515R6 (BRSTNOT04), 2331103R6 (COLNNOT11), 2614153H1 (GBLANOT01), 2656691F6 (LUNGTUT09), 3951176H1 (DRGCNOT01)
129	263	2655184	THYMNOT04	2655184H1 (THYMNOT04), SBDA05215F1, SBDA05213F1, SBDA01516F1
130	264	2848362	BRSTTUT13	1297974F1 and 1297974T6 (BRSTNOT07), 2630138F6 (COLNTUT15), 2848362H1 (BRSTTUT13)
131	265	2849906	BRSTTUT13	1541617R1 and 1541617T1 (SINTTUT01), 2684504F6 and 2684504T6 (LUNGNOT23), 2796805H1 (NPOLNOT01), 2849906H1 (BRSTTUT13)
132	266	2899137	DRGCNOT01	2899137H1 (DRGCNOT01), 3026490F6 and 3026490T6 (HEARFET02), 3483359H1 (KIDNNOT31)
133	267	2986229	CARGDIT01	1740227T6 (HIPONON01), 2986229H1 (CARGDIT01)
134	268	3222081	COLNNON03	1754079F6 (LIVRTUT01), 3222081H1 (COLNNON03), 4053813T6 (SPLNNOT13), 4230282H1 (BRAMDIT01), SBDA07029F3

TABLE 2

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
1	88	T83 S38 T76		M1 - A21		Signal Peptide HMM
2	128	S30 S40 T47 T119 W125		M1 - F28		Signal Peptide HMM
3	111	T70		M1 - T18		Signal Peptide HMM
4	110	S32 T64	N58	M1 - A29		Signal Peptide HMM
5	78	T27 S39 S39 S44 S22 T27 S28 S57		M1 - R24		Signal Peptide HMM
6	88	T55 S30 S40 T55	N34	M1 - N21		Signal Peptide HMM
7	227	S220 S70 S83 T131 S134 S141 T158 Y123	N100	M1 - Q20		Signal Peptide HMM
8	198	S62 T123 S142 S189 S62 T100 Y85	N60	M1 - A28		Signal Peptide HMM
9	65	T48		M1 - A29		Signal Peptide HMM
10	154			M1 - A29		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
11	237	T116 T26 T79 T85 T182 T188 T194 T206 S60 S123 S176 S213	N128	M1 - A19		Signal Peptide HMM
12	225	T158 S128	N166	M1 - G27		Signal Peptide HMM
13	117	S41		M1 - A23		Signal Peptide HMM
14	253	S49 T63 S92 T110 S127 T239	N42 N47 N72 N207	M1 - T20		Signal Peptide HMM
15	171	S43 S94 T114		M88 - R112		Signal Peptide HMM
16	78	S38 S43	N37	M1 - G19		Signal Peptide HMM
17	71	T64 T67		M1 - C19		Signal Peptide HMM
18	188	S36 T58 T133 Y31	N121 N171	M1 - A21		Signal Peptide HMM
19	80	S76		M1 - C19		Signal Peptide HMM
20	80			M1 - G25		Signal Peptide HMM
21	84	S39 S53 S60		M1 - G21		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
22	171	S41 T150		M3 - A21		Signal Peptide HMM
23	243	S3 S44 T75 S86 S183 S223 S36 S92 S205 Y40 Y110	N97	M1 - C25		Signal Peptide HMM
24	311	T5 S76 T82 T93 T109 S121 T137 T170 S184 S11 T53 S75 S84 T132 S223 S274 Y69	N49 N91 N108 N128 N135 N190	M1 - A32		Signal Peptide HMM
25	57			M1 - L29		Signal Peptide HMM
26	82	S46 Y26		M1 - S18		Signal Peptide HMM
27	115			M1 - G34		Signal Peptide HMM
28	327	S93 S50 S167 S233 S89 T105 T214 S302 T318	N138 N206	M1 - E25		Signal Peptide HMM
29	133	S63	N105	M1 - E29		Signal Peptide HMM
30	129	S21 S65 T93		M1 - G20		Signal Peptide HMM

TABLE 2

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
1	88	T83 S38 T76		M1 - A21		Signal Peptide HMM
2	128	S30 S40 T47 T119 W125		M1 - F28		Signal Peptide HMM
3	111	T70		M1 - T18		Signal Peptide HMM
4	110	S32 T64	N58	M1 - A29		Signal Peptide HMM
5	78	T27 S39 S39 S44 S22 T27 S28 S57		M1 - R24		Signal Peptide HMM
6	88	T55 S30 S40 T55	N34	M1 - N21		Signal Peptide HMM
7	227	S220 S70 S83 T131 S134 S141 T158 Y123	N100	M1 - Q20		Signal Peptide HMM
8	198	S62 T123 S142 S189 S62 T100 Y85	N60	M1 - A28		Signal Peptide HMM
9	65	T48		M1 - A29		Signal Peptide HMM
10	154			M1 - A29		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
11	237	T116 T26 T79 T85 T182 T188 T194 T206 S60 S123 S176 S213	N128	M1 - A19		Signal Peptide HMM
12	225	T158 S128	N166	M1 - G27		Signal Peptide HMM
13	117	S41		M1 - A23		Signal Peptide HMM
14	253	S49 T63 S92 T110 S127 T239	N42 N47 N72 N207	M1 - T20		Signal Peptide HMM
15	171	S43 S94 T114		M88 - R112		Signal Peptide HMM
16	78	S38 S43	N37	M1 - G19		Signal Peptide HMM
17	71	T64 T67		M1 - C19		Signal Peptide HMM
18	188	S36 T58 T133 Y31	N121 N171	M1 - A21		Signal Peptide HMM
19	80	S76		M1 - C19		Signal Peptide HMM
20	80			M1 - G25		Signal Peptide HMM
21	84	S39 S53 S60		M1 - G21		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
22	171	S41 T150		M3 - A21		Signal Peptide HMM
23	243	S3 S44 T75 S86 S183 S223 S36 S92 S205 Y40 Y110	N97	M1 - C25		Signal Peptide HMM
24	311	T5 S76 T82 T93 T109 S121 T137 T170 S184 S11 T53 S75 S84 T132 S223 S274 Y69	N49 N91 N108 N128 N135 N190	M1 - A32		Signal Peptide HMM
25	57			M1 - L29		Signal Peptide HMM
26	82	S46 Y26		M1 - S18		Signal Peptide HMM
27	115			M1 - G34		Signal Peptide HMM
28	327	S93 S50 S167 S233 S89 T105 T214 S302 T318	N138 N206	M1 - E25		Signal Peptide HMM
29	133	S63	N105	M1 - E29		Signal Peptide HMM
30	129	S21 S65 T93		M1 - G20		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
31	472	S164 T32 S42 T141 T154 S155 T235 T262 T271 T334 T376 S402 S421 S435 T441 S19 S29 T327 S378	N61 N179 N353 N356 N396	M1 - G20	hematopoietic lineage switch 2 (g3169729)	Signal Peptide HMM BLAST - GenBank
32	93	T21		M1 - A18		Signal Peptide HMM
33	92	S57 S5		M1 - G47		SPScan
34	143	T6 T14 T135		M9 - G40		Signal Peptide HMM
35	89	T15 S58 S66		M1 - A19		Signal Peptide HMM
36	560	T7 T76 S150 T224 S228 S257 S358 S474 S529 S539 T186 S219 S368 Y523	N163 N184 N379	M1 - E34		SPScan
37	197	T80 S163		M1 - G28		Signal Peptide HMM
38	437	T47 T146 S233 S391 S403 T43 S130 S273 S339 S364	N46 N189 N382	M1 - A21		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
39	330	S197 T49 T150 S193 T214 T215 T49 S111 S237	N46 N64 N166 N191	M1 - G28		Signal Peptide HMM
40	148	T73 S141	N29 N58 N71 N103	M1 - R24	receptor-activity-modifying protein (RAMP; g4165368)	Signal Peptide HMM BLAST - GenBank
41	188	S49		M1 - V25		Signal Peptide HMM
42	222	S89 S165 T174 T182 T83 S155		M1 - S24		Signal Peptide HMM
43	111	S54 S29 S98 S50 S57 T104		M1 - T23		Signal Peptide HMM
44	341	T29 S106 T120 S161 S195 S37 S47 T51 S136 S223 S230 S281		M1 - G22		Signal Peptide HMM
45	148	S21 T63 T63 A146	N40	M1 - G23		Signal Peptide HMM
46	87	S65		M1 - P18		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
47	383	T77 S95 S108 S280 S351 S121 S124 S153 T187	N93 N207	M1 - P23		Signal Peptide HMM
48	109	S25 S22		M1 - L18		Signal Peptide HMM
49	185	S62		M1 - A20		Signal Peptide HMM
50	110	T100 T73 S97 Y48	N71	M1 - C21		Signal Peptide HMM
51	126	S17 S110		M1 - G18		Signal Peptide HMM
52	488	S205 T31 S86 T236 S7 T447	N250 N321 N463	M1 - L25	putative involvement in cell wall structure or biosynthesis (g3738170)	Signal Peptide HMM BLAST - GenBank
53	197	T55 S34 S46 S69 T98 S108 T119 T167 S194 S2 S34 T153		M1 - A26		Signal Peptide HMM
54	84	S65 S36 T41 S51 S69 S81	N39	M1 - G25		Signal Peptide HMM
55	97	S56		M1 - A22		Signal Peptide HMM
56	140	S29		M1 - P23		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
57	285	S53 S108 T216 S253 S277	N153	M1 - A25		Signal Peptide HMM
58	262	S62 T166 S62 S71 Y246	N190	M1 - G28	3-acylating enzyme (Q44449)	Signal Peptide HMM BLAST - GENESEQ
59	189	S120 T154 T34 T37 S174		M1 - C22		Signal Peptide HMM
60	257	S98 T136 T67 S112 S234 S237		M55 - E84B		SPScan
61	82	T68	N67	M1 - G18		Signal Peptide HMM
62	202	T21 S117 S120		M1 - G27		Signal Peptide HMM
63	450	S107 S97 S146 S339 S440 S245 T303 S304 S399		M1 - G18		Signal Peptide HMM
64	322	T145 T214 T16 S24 S35 S45 T145 T269 S297 T300 T314 Y87	N53 N130 N289	M1 - G23		Signal Peptide HMM
65	104	S38 S25 S75		M1 - A18		Signal Peptide HMM

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
66	93			M1 through about S18 Transmembrane: M1 through about Y17		SPscan HMM
67	71	S23 S64		M1 through about A24		SPscan HMM MOTIFS
68	394	S392 S393 S31 S127 S179 S334 T338 S358 T383 Y323	N53	M1 through about S31 Transmembrane: about M159 through about F178 about F109 through about S127 about F225 through about V243		SPScan HMM MOTIFS
69	72	S59	N69	M1 through about S23 Transmembrane: M1 through about L16		SPscan HMM MOTIFS
70	71	S11 T26		M1 through about Q18		SPscan HMM MOTIFS
71	247	S41 T79		M1 through about S25		SPscan HMM MOTIFS
72	73	S56		M1 through about G27		SPscan HMM MOTIFS

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
73	70			M1 through about G20		SPscan HMM
74	67			M1 through about G30		SPscan HMM
75	91			M1 through about G26		SPScan
76	56	T29 S46 T51		M1 through about S19		SPscan HMM MOTIFS
77	112	S62 S65		M1 through about G27 Transmembrane: about W79 through about H97		SPscan HMM MOTIFS
78	54		N48	M1 through about N34		SPscan HMM MOTIFS
79	57	T33 R55		M1 through about C18		SPscan HMM MOTIFS
80	52	S34		M1 through about S30		SPscan HMM MOTIFS

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
81	64	T43 Y27		M1 through about S41		SPscan HMM MOTIFS
82	65	S45		M1 through about A31 Transmembrane: about L38 through about F55		SPscan HMM MOTIFS
83	56			M1 through about E23		SPscan HMM
84	120	S69 S109	N89 N95	M1 through about A38 Transmembrane: about L23 through about T41		SPscan HMM MOTIFS
85	67	S28		M1 through about K30 Microbodies C-terminal targeting signal: A65KV		SPscan HMM MOTIFS
86	62	S29 S42 S46	N40	M1 through about S29		SPscan HMM MOTIFS
87	75	S25 S46		M1 through about L19 Transmembrane: about I3 through about G20		SPscan HMM MOTIFS

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
88	80	T28		M1 through about A20		SPscan HMM MOTIFS
89	50	S11		M1 through about C48		SPscan HMM MOTIFS
90	116	S38		M1 through about G22		SPscan HMM MOTIFS
91	67	S43		M1 through about P21		SPscan HMM MOTIFS
92	538	S415 S52 T77 S97 T178 T228 S282 S320 S332 S384 T401 T424 S483 S207 S230 S357 T410 Y263 Y365	N226	M1 through about S18 Tyrosine specific protein phosphatases signature: about V328 through about F340		SPscan BLOCKS PRINTS MOTIFS
93	58			M1 through about S25		SPscan HMM
94	119	S39		M1 through about S22 Transmembrane: about V3 through about S21		SPscan HMM MOTIFS

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
95	128	S91		M1 through about G31 Transmembrane: about F108 through about L126		SPScan HMM MOTIFS
96	124	T115 T43 S91		M1-S20 P116-V124 (urotensin II signature)		SPScan HMM Motifs BLOCKS BLAST
97	182	S28 T70 S172 S25 S32 S48 S108 S131		M1-S23, M1-S25		SPScan HMM Motifs
98	237	S55 S88 S121 S135	N45 N73 N107 N118 N132 N172 N175 N185	M1-A16, M1-S21 C40-C198 (cysteine spacing pattern similar to that of RoBo-1)		SPScan HMM Motifs BLAST
99	160	S36 S59 T143		M1-A27		SPScan HMM Motifs
100	148	T76 S64 Y103		M1-S30, M1-G31		SPScan HMM Motifs
101	170	S78 T4 T30 S130 S25 S29 T122		M1-A23, M1-L28		SPScan HMM Motifs

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
102	150	S50 S78 S91		M1-A26, M1-S28		SPScan HMM Motifs
103	142	T57 T80		M1-A25, M1-G26		SPScan HMM Motifs
104	110	T3		M1-G18, M1-T25		SPScan HMM Motifs
105	120	T29 S40 S72		M1-G22, M1-A20		SPScan HMM Motifs
106	135	T115 S38 T41	N32 N101	M1-G26, M1-C25		SPScan HMM Motifs
107	301	S53 S217 S240 S283 T224		M1-A22		SPScan HMM Motifs
108	103	S88 T73 S84		M1-P19, M1-L22		SPScan HMM Motifs
109	95	T82 S52 S77	N50	M1-T15, M1-P19		SPScan HMM Motifs

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
110	113	T84 S4		M1-P19, M1-A24		SPScan HMM Motifs
111	234	S179 S184 S51 T70 T158 S168 T228 Y29	N146 N191 N194	M1-A20	NK cell activating receptor (g4493702)	SPScan HMM Motifs BLAST - GenBank
112	119	S39 T61		M1-G30, M1-G27		SPScan HMM Motifs
113	200	S51 T46 S191		M1-G26 Signal Peptide	Signal Peptide Containing Protein, Homology with KIAA0206	SPScan Motifs BLAST
114	225			M1-Q29 Signal Peptide	Signal Peptide Containing Protein	SPScan
115	155	S29		M1-A20 Signal Peptide	Signal Peptide Containing Protein	HMM Motifs
116	468	S143 T156 T227 S235 T271 T293 T436 S453 S117 T148 T213 S263 S417 Y73	N280 N384	M1-G23 Signal Peptide	Signal Peptide Containing Protein	SPScan Motifs
117	403	S19 S320 S69 S151 T171 T97 S393 Y193 Y378	N87	M1-A24 Signal Peptide	Signal Peptide Containing Protein	HMM Motifs

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
118	131	T131 S24 T79 T118 T123 T127	N116	M1-G25 Signal Peptide	Signal Peptide Containing Protein	SPScan Motifs
119	556	T176 S192 S196 T220 S344 S369 S476 T501 S529 S541 T548 T553 S48 S115 S121 T386 T424 S500 Y104	N62 N79 N127 N157 N160	M1-P21 Signal Peptide L226-W244, Y402-W422, V375-L392 and Y355-I376 Transmembrane Domains	Signal Peptide Containing Protein, Weakly similar to Putative Transmembrane Protein (PTM1) Precursor	SPScan Motifs HMM BLAST
120	514	T457 T80 S86 T141 T372 T420 S447 S94 T102 S112 T240 S297 S353 S470	N100 N168 N319	M1-G24 Signal Peptide	Signal Peptide Containing Protein,	SPScan Motifs
121	109	T46 S78 T12		M1-S15 Signal Peptide	Signal Peptide Containing Protein	SPScan Motifs
122	431	S57 T320 S339 S396 S100 S239		M1-L25 Signal Peptide	Signal Peptide Containing Protein, Weakly similar to OXA1L	SPScan Motifs BLAST
123	142			M1-W16 Signal Peptide	Signal Peptide Containing Protein	SPScan

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
124	643	T8 S28 S77 T169 T199 T235 S252 T320 S402 T413 S414 S558 S22 T25 S56 S62 S120 T184 S329 T423 S475 S574 Y226	N251	M1-S28 Signal Peptide, D37-C81, W380-C437, W440- C492 and F526-C583 Thrombospondin Type I Domains	Signal Peptide Containing Protein, Thrombospondin Type I Protein	SPScan Motifs Pfam BLAST
125	568	S510 T24 T80 S91 T153 T165 S232 S248 S262 T300 T334 S380 S446 S16 T19 T60 S127 S273 T436 T531 S554 T564 Y135 Y489	N322	M1-T19 Signal Peptide	Signal Peptide Containing Protein	SPScan Motifs
126	125	T62 S27 T36		M1-R32 Signal Peptide, V4-L53 Glycosyl Hydrolase Family 9 Active Site Signature	Signal Peptide Containing Protein, Glycosyl Hydrolase Protein	SPScan Motifs PROFILE- SCAN
127	196	T105 T47 T56 S158		M1-S26 Signal Peptide, H79-H123 Ribosomal Protein S18 Signature	Signal Peptide Containing Protein, Ribosomal Protein S18	SPScan Motifs BLAST Pfam PROFILE- SCAN
128	214	S112 S131	N37 N92	M1-S35 Signal Peptide	Signal Peptide Containing Protein, Homology with GTP Binding Protein	SPScan Motifs BLAST

TABLE 2 (cont.)

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences	Identification	Analytical Methods
129	88			M1-S24 Signal Peptide	Signal Peptide Containing Protein	HMM
130	260	S146 S179 S192 S239 S70 T126 T150	N50 N109	M1-A48 Signal Peptide, G59-S142 Immunoglobulin Domain	Signal Peptide Containing Protein, Immunoglobulin Superfamily Protein	SPScan Motifs Pfam
131	295	T176 T56 S72 S179 S256 S87		M1-A30 Signal Peptide	Signal Peptide Containing Protein	SPScan Motifs
132	183	S11 T41 T42 S83		M1-W24 Signal Peptide, E131-K168 and C105-H115 Adrenodoxin Iron-Sulfur Binding Signature, C111-V116 Cytochrome C Heme Binding Signature, N69-A162 Iron-Sulfur Cluster Binding Domain	Signal Peptide Containing Protein, Adrenodoxin Family Iron-Sulfur Binding Protein, and Cytochrome C Family Heme Binding Protein	HMM Motifs BLOCKS PRINTS Pfam
133	113	S93 T89 Y9		M1-G30 Signal Peptide, V28-L74 PF00646 F-Box Domain	Signal Peptide Containing Protein, PF00646 F-Box Protein	SPScan Motifs Pfam
134	160	T46 T55 S65 S124 T125 T46		M1-A27 Signal Peptide	Signal Peptide Containing Protein, F45G2.10 and Yhr122wp Homology	SPScan Motifs BLAST

TABLE 3

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
135	Hematopoietic/Immune (1.000)	Inflammation (1.000)	pBLUESCRIPT
136	Hematopoietic/Immune (0.750) Cardiovascular (0.250)	Inflammation (0.750) Cancer (0.250)	pSPORT1
137	Nervous (1.000)	Trauma (1.000)	pSPORT1
138	Musculoskeletal (1.000)	Inflammation (1.000)	pSPORT1
139	Gastrointestinal (0.714) Cardiovascular (0.143) Reproductive (0.143)	Cancer (0.714) Trauma (0.143)	pSPORT1
140	Nervous (1.000)	Neurological (0.500) Trauma (0.500)	pSPORT1
141	Reproductive (0.293) Gastrointestinal (0.146) Hematopoietic/Immune (0.146)	Cancer (0.524) Inflammation (0.256) Fetal (0.146)	pSPORT1
142	Reproductive (0.266) Gastrointestinal (0.170) Nervous (0.138)	Cancer (0.479) Inflammation (0.277) Fetal (0.181)	pINCY
143	Reproductive (0.417) Nervous (0.292) Developmental (0.125)	Cancer (0.417) Inflammation (0.250) Fetal (0.167)	pINCY
144	Reproductive (0.321) Cardiovascular (0.143) Developmental (0.143)	Cancer (0.464) Fetal (0.214) Inflammation (0.143)	pINCY
145	Reproductive (0.600) Gastrointestinal (0.400)	Cancer (0.400) Trauma (0.400) Inflammation (0.200)	pINCY
146	Cardiovascular (0.400) Dermatologic (0.200) Nervous (0.200)	Cancer (0.600) Fetal (0.600)	pINCY
147	Developmental (0.667) Gastrointestinal (0.333)	Fetal (0.667) Cancer (0.333)	pINCY
148	Reproductive (0.256) Nervous (0.248) Cardiovascular (0.137)	Cancer (0.479) Inflammation (0.214) Fetal (0.145)	pINCY
149	Reproductive (0.244) Nervous (0.178) Hematopoietic/Immune (0.167)	Cancer (0.433) Inflammation (0.322) Fetal (0.156)	pINCY

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
150	Cardiovascular (0.923) Developmental (0.077)	Cancer (0.692) Fetal (0.154) Inflammation (0.154)	pINCY
151	Reproductive (0.215) Nervous (0.190) Gastrointestinal (0.177)	Cancer (0.494) Inflammation (0.278) Trauma (0.152)	pINCY
152	Reproductive (0.200) Nervous (0.171) Hematopoietic/Immune (0.143)	Inflammation (0.371) Cancer (0.229) Fetal (0.200)	pINCY
153	Reproductive (0.333) Nervous (0.157) Hematopoietic/Immune (0.137)	Cancer (0.549) Inflammation (0.176) Fetal (0.137)	pINCY
154	Gastrointestinal (0.500) Urologic (0.167)	Inflammation (0.667) Cancer (0.167) Trauma (0.167)	pINCY
155	Gastrointestinal (0.429) Reproductive (0.286) Nervous (0.143)	Inflammation (0.429) Cancer (0.286) Trauma (0.143)	pINCY
156	Reproductive (1.000)	Cancer (0.500) Inflammation (0.500)	pINCY
157	Hematopoietic/Immune (0.346) Reproductive (0.154) Gastrointestinal (0.115)	Cancer (0.404) Inflammation (0.404) Fetal (0.212)	pINCY
158	Reproductive (0.236) Hematopoietic/Immune (0.217) Gastrointestinal (0.132)	Cancer (0.415) Inflammation (0.358) Fetal (0.142)	pINCY
159	Gastrointestinal (1.000)	Cancer (1.000)	pSPORT1
160	Developmental (0.500) Hematopoietic/Immune (0.250) Nervous (0.250)	Fetal (0.500) Inflammation (0.250) Trauma (0.250)	pINCY
161	Hematopoietic/Immune (0.250) Reproductive (0.250) Nervous (0.208)	Cancer (0.583) Fetal (0.292) Inflammation (0.250)	pINCY
162	Gastrointestinal (0.412) Reproductive (0.412) Cardiovascular (0.088)	Cancer (0.735) Inflammation (0.176) Fetal (0.029)	pINCY

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
163	Reproductive (0.298) Cardiovascular (0.170) Nervous (0.149)	Cancer (0.532) Inflammation (0.213) Fetal (0.191)	pINCY
164	Gastrointestinal (0.333) Hematopoietic/Immune (0.333) Reproductive (0.333)	Cancer (0.667) Inflammation (0.333)	pINCY
165	Reproductive (0.295) Gastrointestinal (0.159) Nervous (0.148)	Cancer (0.534) Inflammation (0.284) Fetal (0.091)	pINCY
166	Hematopoietic/Immune (0.538) Cardiovascular (0.077) Reproductive (0.077)	Inflammation (0.731) Cancer (0.154) Fetal (0.154)	pINCY
167	Reproductive (0.483) Gastrointestinal (0.121) Nervous (0.103)	Cancer (0.672) Inflammation (0.155)	pINCY
168	Gastrointestinal (0.222) Hematopoietic/Immune (0.222) Nervous (0.148)	Cancer (0.519) Inflammation (0.370) Fetal (0.259)	pINCY
169	Urologic (1.000)	Cancer (0.333) Fetal (0.333) Inflammation (0.333)	pINCY
170	Reproductive (0.214) Gastrointestinal (0.179) Nervous (0.143)	Cancer (0.643) Inflammation (0.143) Fetal (0.107)	pINCY
171	Reproductive (0.261) Developmental (0.174) Nervous (0.174)	Cancer (0.391) Fetal (0.304) Inflammation (0.217)	pINCY
172	Reproductive (0.357) Gastrointestinal (0.321) Cardiovascular (0.071)	Cancer (0.571) Inflammation (0.286) Fetal (0.107)	pINCY
173	Reproductive (0.306) Nervous (0.161) Cardiovascular (0.129)	Cancer (0.387) Inflammation (0.323) Fetal (0.226)	pINCY
174	Reproductive (0.229) Nervous (0.188) Cardiovascular (0.167)	Cancer (0.521) Inflammation (0.312) Trauma (0.146)	pSPORT1

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
175	Reproductive (0.444) Developmental (0.167) Cardiovascular (0.111)	Cancer (0.556) Fetal (0.278) Trauma (0.111)	pSPORT1
176	Reproductive (0.294) Gastrointestinal (0.176) Cardiovascular (0.118)	Cancer (0.765) Fetal (0.118) Inflammation (0.118)	pSPORT1
177	Gastrointestinal (1.000)	Cancer (0.667) Inflammation (0.333)	pINCY
178	Reproductive (0.385) Nervous (0.231) Gastrointestinal (0.154)	Cancer (0.385) Inflammation (0.385)	pINCY
179	Reproductive (0.500) Cardiovascular (0.167) Gastrointestinal (0.167)	Cancer (0.667) Fetal (0.167) Inflammation (0.167)	pBLUESCRIPT
180	Cardiovascular (0.231) Reproductive (0.231) Gastrointestinal (0.154)	Cancer (0.615) Inflammation (0.308) Fetal (0.154)	pINCY
181	Reproductive (0.324) Gastrointestinal (0.176) Cardiovascular (0.130)	Cancer (0.519) Inflammation (0.222) Fetal (0.157)	pINCY
182	Reproductive (0.320) Nervous (0.180) Gastrointestinal (0.120)	Cancer (0.580) Inflammation (0.160) Fetal (0.100)	pINCY
183	Gastrointestinal (0.667) Reproductive (0.333)	Cancer (1.000)	pINCY
184	Urologic (0.667) Dermatologic (0.333)	Cancer (0.667) Fetal (0.333)	pSPORT1
185	Cardiovascular (0.500) Reproductive (0.500)	Cancer (1.000)	pINCY
186	Reproductive (0.393) Developmental (0.107) Urologic (0.107)	Cancer (0.607) Fetal (0.179) Inflammation (0.107)	pINCY
187	Cardiovascular (0.400) Reproductive (0.333) Gastrointestinal (0.133)	Inflammation (0.467) Cancer (0.267) Fetal (0.267)	pSPORT1
188	Nervous (0.318) Reproductive (0.227) Urologic (0.136)	Cancer (0.636) Inflammation (0.136) Trauma (0.091)	pINCY

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
189	Cardiovascular (0.500) Reproductive (0.500)	Cancer (1.000)	pINCY
190	Reproductive (0.318) Nervous (0.227) Hematopoietic/Immune (0.136)	Cancer (0.500) Fetal (0.227) Inflammation (0.227)	pINCY
191	Reproductive (0.253) Cardiovascular (0.158) Gastrointestinal (0.147)	Cancer (0.463) Inflammation (0.232) Fetal (0.200)	pINCY
192	Reproductive (0.333) Gastrointestinal (0.286) Cardiovascular (0.095)	Cancer (0.571) Inflammation (0.333) Fetal (0.095)	pINCY
193	Reproductive (0.304) Cardiovascular (0.217) Gastrointestinal (0.130)	Cancer (0.435) Inflammation (0.391) Fetal (0.174)	pINCY
194	Reproductive (0.312) Nervous (0.188) Cardiovascular (0.125)	Cancer (0.438) Inflammation (0.250) Fetal (0.188)	pINCY
195	Developmental (1.000)	Fetal (1.000)	pINCY
196	Reproductive (0.233) Cardiovascular (0.209) Nervous (0.140)	Cancer (0.605) Fetal (0.186) Inflammation (0.116)	pINCY
197	Reproductive (0.182) Gastrointestinal (0.136) Hematopoietic/Immune (0.136)	Cancer (0.477) Inflammation (0.341) Fetal (0.182)	pINCY
198	Gastrointestinal (0.205) Reproductive (0.205) Cardiovascular (0.114)	Inflammation (0.341) Cancer (0.250) Fetal (0.227)	pINCY
199	Cardiovascular (0.520) Reproductive (0.280) Developmental (0.160)	Cancer (0.720) Fetal (0.200) Inflammation (0.080)	pINCY
200	Lung (0.958) Developmental (0.25) Musculoskeletal (0.042)	Cancer (0.583) Fetal or Proliferating (0.292) Inflammation (0.167)	pBLUESCRIPT
201	Reproductive (0.571) Musculoskeletal (0.143) Nervous (0.143) Urologic (0.143)	Cancer (0.429) Inflammation (0.571)	pSPORT1

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
202	Endocrine (0.250) Nervous (0.250) Cardiovascular (0.125) Developmental (0.125) Gastrointestinal (0.125) Reproductive (0.125)	Cancer (0.375) Inflammation (0.625) Fetal or Proliferating (0.125)	pSPORT1
203	Lung (1.000)	Fetal or Proliferating (1.000)	pINCY
204	Lung (0.500) Penis (0.500)	Cancer (0.500)	pINCY
205	Cardiovascular (0.231) Dermatologic (0.231) Reproductive (0.231)	Fetal or Proliferating (0.385) Cancer (0.308)	pINCY
206	Nervous (0.596) Reproductive (0.154) Gastrointestinal (0.077)	Cancer (0.442) Neurological (0.192) Inflammation (0.231)	pINCY
207	Gastrointestinal (1.000)	Inflammation (1.000)	pINCY
208	Reproductive (0.300) Hematopoietic/Immune (0.200) Nervous (0.150)	Cancer (0.450) Inflammation (0.400) Fetal or Proliferating (0.250)	pSPORT1
209	Heart (0.500) Brain (0.500)	Neurological (0.500) Inflammation (0.500)	pINCY
210	Nervous (0.625) Reproductive (0.250) Musculoskeletal (0.125)	Cancer (0.750) Fetal or Proliferating (0.250) Neurological (0.125)	pINCY
211	Nervous (0.261) Reproductive (0.304) Gastrointestinal (0.174)	Cancer (0.522) Fetal or Proliferating (0.174) Inflammation (0.130)	pSPORT1
212	Testis (1.000)	Inflammation (1.000)	pBLUESCRIPT
213	Nervous (0.400) Reproductive (0.400) Gastrointestinal (0.200)	Cancer (0.400) Inflammation (0.400) Neurological (0.200)	pBLUESCRIPT
214	Reproductive (0.476) Gastrointestinal (0.286) Cardiovascular (0.095)	Cancer (0.714) Inflammation (0.286) Neurological (0.048)	pSPORT1

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
215	Reproductive (0.284) Gastrointestinal (0.216) Nervous (0.176) Hematopoietic/Immune (0.108) Cardiovascular (0.108)	Cancer (0.486) Inflammation (0.351) Fetal or Proliferating (0.122)	pSPORT1
216	Uterus (0.500) Prostate (0.500)	Cancer (0.500) Inflammation (0.500)	pINCY
217	Nervous (0.429) Cardiovascular (0.143) Gastrointestinal (0.143) Hematopoietic/Immune (0.143) Reproductive (0.143)	Cancer (0.571) Inflammation (0.429) Fetal or Proliferating (0.285)	pSPORT1
218	Reproductive (0.450) Hematopoietic/Immune (0.200) Nervous (0.100) Gastrointestinal (0.100)	Cancer (0.650) Inflammation (0.200) Fetal or Proliferating (0.050)	pINCY
219	Reproductive (0.364) Cardiovascular (0.182) Nervous (0.182)	Cancer (0.636) Fetal or Proliferating (0.182) Inflammation (0.273)	pINCY
220	Prostate (1.000)	Inflammation (1.000)	pSPORT1
221	Developmental (0.333) Nervous (0.333) Reproductive (0.333)	Cancer (0.667) Fetal or Proliferating (0.667)	pSPORT1
222	Reproductive (0.393) Hematopoietic/Immune (0.180) Nervous (0.098) Cardiovascular (0.098)	Cancer (0.508) Inflammation (0.344) Fetal or Proliferating (0.066)	pSPORT1
223	Endocrine (0.333) Gastrointestinal (0.333) Reproductive (0.333)	Cancer (1.000)	pINCY
224	Cardiovascular (0.200) Developmental (0.200) Gastrointestinal (0.200) Reproductive (0.200) Urologic (0.200)	Cancer (0.800) Fetal or Proliferating (0.200)	pINCY
225	Lung (1.000)	Cancer (1.000)	pINCY
226	Reproductive (0.302) Hematopoietic/Immune (0.254) Cardiovascular (0.111)	Cancer (0.381) Inflammation (0.381) Fetal or Proliferating (0.286)	pSPORT1

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
227	Lymphocytes (1.000)	Inflammation (1.000)	pINCY
228	Cardiovascular (0.531) Reproductive (0.250) Urologic (0.094)	Cancer (0.656) Inflammation (0.250) Fetal or Proliferating (0.094)	pINCY
229	Reproductive (0.333) Cardiovascular (0.167) Gastrointestinal (0.167) Endocrine (0.167) Hematopoietic/Immune (0.167)	Cancer (0.500) Fetal or Proliferating (0.167) Inflammation (0.333)	pINCY
230	Hematopoietic/Immune (0.500) Reproductive (0.500)	Cell Proliferation (0.500) Inflammation (0.500)	pBLUESCRIPT
231	Cardiovascular (0.333) Nervous (0.333) Developmental (0.167)	Cancer (0.500) Cell Proliferation (0.333) Inflammation (0.167)	pINCY
232	Gastrointestinal (0.938) Reproductive (0.062)	Cancer (0.500) Inflammation (0.500)	pINCY
233	Nervous (0.324) Reproductive (0.235) Hematopoietic/Immune (0.118)	Cancer (0.456) Inflammation (0.235) Trauma (0.147)	pINCY
234	Nervous (0.255) Reproductive (0.255) Musculoskeletal (0.182)	Cancer (0.545) Inflammation (0.255) Trauma (0.109)	pINCY
235	Musculoskeletal (0.308) Reproductive (0.231) Gastrointestinal (0.154)	Cancer (0.538) Inflammation (0.231) Trauma (0.154)	pINCY
236	Nervous (1.000)	Cancer (1.000)	pINCY
237	Gastrointestinal (0.429) Hematopoietic/Immune (0.143) Nervous (0.143)	Cancer (0.571) Cell Proliferation (0.143) Trauma (0.143)	pINCY
238	Reproductive (0.254) Gastrointestinal (0.160) Nervous (0.128)	Cancer (0.453) Inflammation (0.241) Cell Proliferation (0.175)	pINCY
239	Nervous (0.333) Dermatologic (0.167) Endocrine (0.167)	Trauma (0.333) Cancer (0.167) Cell Proliferation (0.167)	pINCY

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
240	Nervous (0.273) Reproductive (0.227) Endocrine (0.136)	Cancer (0.545) Cell Proliferation (0.182) Inflammation (0.182)	pINCY
241	Reproductive (0.273) Hematopoietic/Immune (0.182) Urologic (0.182)	Cancer (0.455) Cell Proliferation (0.273) Inflammation (0.273)	pINCY
242	Endocrine (1.000)	Trauma (1.000)	pSPORT1
243	Reproductive (1.000)	Cancer (1.000)	pINCY
244	Hematopoietic/Immune (0.545) Musculoskeletal (0.182) Cardiovascular (0.091)	Inflammation (0.636) Trauma (0.182) Cancer (0.091)	pINCY
245	Hematopoietic/Immune (0.400) Musculoskeletal (0.300) Cardiovascular (0.150)	Inflammation (0.650) Cancer (0.300)	pINCY
246	Urologic (1.000)	Cancer (0.500) Cell Proliferation (0.500)	pINCY
247	Nervous (0.292) Reproductive (0.222) Musculoskeletal (0.125)	Cell Proliferation (0.625) Inflammation/Trauma (0.181)	pSPORT1
248	Reproductive (0.211) Developmental (0.132) Nervous (0.132)	Cell Proliferation (0.658) Inflammation/Trauma (0.184)	pSPORT1
249	Nervous (0.500) Gastrointestinal (0.300) Hematopoietic/Immune (0.100)	Cell Proliferation (0.900) Inflammation/Trauma (0.300)	pSPORT1
250	Cardiovascular (0.209) Gastrointestinal (0.140) Hematopoietic/Immune (0.140)	Cell Proliferation (0.605) Inflammation/Trauma (0.256)	pINCY
251	Nervous (0.308) Cardiovascular (0.154) Gastrointestinal (0.154)	Cell Proliferation (0.616) Inflammation/Trauma (0.269)	pINCY
252	Reproductive (1.000)	Cell Proliferation (1.000)	pSPORT1

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
253	Reproductive (0.324) Nervous (0.162) Gastrointestinal (0.113)	Cell Proliferation (0.641) Inflammation/Trauma (0.197)	pSPORT1
254	Reproductive (0.315) Nervous (0.296) Developmental (0.093)	Cell Proliferation (0.630) Inflammation/Trauma (0.278)	pSPORT1
255	Nervous (0.211) Reproductive (0.211) Gastrointestinal (0.158)	Cell Proliferation (0.579) Inflammation/Trauma (0.298)	pINCY
256	Reproductive (0.250) Gastrointestinal (0.148) Hematopoietic/Immune (0.148)	Cell Proliferation (0.705) Inflammation/Trauma (0.193)	pINCY
257	Hematopoietic/Immune (1.000)	Cell Proliferation (0.400) Inflammation/Trauma (0.600)	pINCY
258	Cardiovascular (0.333) Reproductive (0.333) Developmental (0.167)	Cell Proliferation (0.833) Inflammation/Trauma (0.333)	pBLUESCRIPT
259	Cardiovascular (0.333) Reproductive (0.250) Developmental (0.167)	Cell Proliferation (0.625) Inflammation/Trauma (0.208)	pINCY
260	Endocrine (0.500) Cardiovascular (0.250) Nervous (0.250)	Cell Proliferation (0.750) Inflammation/Trauma (0.500)	pINCY
261	Reproductive (0.252) Cardiovascular (0.155) Hematopoietic/Immune (0.136)	Cell Proliferation (0.728) Inflammation/Trauma (0.194)	pINCY
262	Reproductive (0.274) Cardiovascular (0.177) Nervous (0.145)	Cell Proliferation (0.742) Inflammation/Trauma (0.210)	pINCY
263	Reproductive (0.267) Cardiovascular (0.160) Hematopoietic/Immune (0.127)	Cell Proliferation (0.654) Inflammation/Trauma (0.193)	pINCY
264	Nervous (0.229) Hematopoietic/Immune (0.200) Reproductive (0.200)	Cell Proliferation (0.743) Inflammation/Trauma (0.286)	pINCY
265	Hematopoietic/Immune (0.333) Gastrointestinal (0.167) Nervous (0.133)	Cell Proliferation (0.600) Inflammation/Trauma (0.333)	pINCY

TABLE 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease/Condition-Specific Expression (Total of Fraction)	Vector
266	Nervous (0.290) Reproductive (0.258) Cardiovascular (0.129)	Cell Proliferation (0.677) Inflammation/Trauma (0.194)	pINCY
267	Reproductive (0.261) Hematopoietic/Immune (0.217) Cardiovascular (0.087)	Cell Proliferation (0.652) Inflammation/Trauma (0.391)	pINCY
268	Gastrointestinal (0.227) Reproductive (0.193) Hematopoietic/Immune (0.168)	Cell Proliferation (0.731) Inflammation/Trauma (0.227)	pSPORT1

TABLE 4

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
135	443531	MPHGN0T03	The library was constructed using RNA isolated from plastic adherent mononuclear cells isolated from buffy coat units obtained from unrelated male and female donors.
136	632860	NEUTGMT01	The library was constructed using RNA isolated from peripheral blood granulocytes collected by density gradient centrifugation through Ficoll-Hypaque. The cells were isolated from buffy coat units obtained from 20 unrelated male and female donors. Cells were cultured in 10 nM GM-CSF for 1 hour before washing and harvesting for RNA preparation.
137	670010	CRBLN0T01	The library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis.
138	726498	SYNOOAT01	The library was constructed using RNA isolated from the knee synovial membrane tissue of an 82-year-old female with osteoarthritis.
139	795064	OVARN0T03	The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, cerebrovascular disease, breast cancer, and uterine cancer.
140	924925	BRAIN0T04	The library was constructed using RNA isolated from the brain tissue of a 44-year-old Caucasian male with a cerebral hemorrhage. The tissue, which contained coagulated blood, came from the choroid plexus of the right anterior temporal lobe. Family history included coronary artery disease and myocardial infarction.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
141	962390	BRSTTUT03	The library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multifentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type I diabetes.
142	1259405	MENITUT03	The library was constructed using RNA isolated from brain meningioma tissue removed from a 35-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a benign neoplasm in the right cerebellopontine angle of the brain. Patient history included hypothyroidism. Family history included myocardial infarction and breast cancer.
143	1297384	BRSTNOT07	The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, atherosclerotic coronary artery disease, and type II diabetes.
144	1299627	BRSTNOT07	The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, atherosclerotic coronary artery disease, and type II diabetes.
145	1306026	PLACNOT02	The library was constructed using RNA isolated from the placental tissue of a Hispanic female fetus, who was prematurely delivered at 21 weeks' gestation. Serologies of the mother's blood were positive for CMV (cytomegalovirus).

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
146	1316219	BLADTUT02	The library was constructed using RNA isolated from bladder tumor tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology indicated grade 3 invasive transitional cell carcinoma. Family history included osteoarthritis and atherosclerosis.
147	1329031	PANCNOT07	The library was constructed using RNA isolated from the pancreatic tissue of a Caucasian male fetus, who died at 23 weeks' gestation.
148	1483050	CORPNOT02	The library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
149	1514160	PANCTUT01	The library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female during radical subtotal pancreatectomy. Pathology indicated an invasive grade 2 adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, benign neoplasm in the large bowel, and a cataract. Family history included cardiovascular disease, type II diabetes, and stomach cancer.
150	1603403	LUNGNOT15	The library was constructed using RNA isolated from lung tissue removed from a 69-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated residual grade 3 invasive squamous cell carcinoma. Patient history included acute myocardial infarction, prostatic hyperplasia, and malignant skin neoplasm. Family history included cerebrovascular disease, type I diabetes, acute myocardial infarction, and arteriosclerotic coronary disease.
151	1652303	PROSTUT08	The library was constructed using RNA isolated from prostate tumor tissue removed from a 60-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated an adenocarcinoma (Gleason grade 3+4). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA). Patient history included a kidney cyst. Family history included tuberculosis, cerebrovascular disease, and arteriosclerotic coronary artery disease.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
152	1693358	COLNNOT23	The library was constructed using RNA isolated from diseased colon tissue removed from a 16-year-old Caucasian male during a total colectomy with abdominal/perineal resection. Pathology indicated gastritis and pancolitis consistent with the acute phase of ulcerative colitis. There was only mild involvement of the ascending and sigmoid colon, and no significant involvement of the cecum, rectum, or terminal ileum. Family history included irritable bowel syndrome.
153	1707711	DUODNOT02	The library was constructed using RNA isolated from duodenal tissue of a 8-year-old Caucasian female, who died from head trauma. Serology was positive for cytomegalovirus (CMV).
154	1738735	COLNNOT22	The library was constructed using RNA isolated from colon tissue removed from a 56-year-old Caucasian female with Crohn's disease during a partial resection of the small intestine. Pathology indicated Crohn's disease of the ileum and ileal-colonic anastomosis, causing a fistula at the anastomotic site that extended into pericolic fat. The ileal mucosa showed linear and punctate ulcers with intervening normal tissue. Previous surgeries included a partial ileal resection and permanent ileostomy. Family history included irritable bowel syndrome.
155	1749147	STOMTUT02	The library was constructed using RNA isolated from stomach tumor tissue obtained from a 68-year-old Caucasian female during a partial gastrectomy. Pathology indicated a malignant lymphoma of diffuse large-cell type. Patient history included thalassemia. Family history included acute leukemia, malignant neoplasm of the esophagus, malignant stomach neoplasm, and atherosclerotic coronary artery disease.
156	1817722	PROSNOT20	The library was constructed using RNA isolated from diseased prostate tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma.
157	1831290	THPIAZT01	The library was constructed using 1 microgram of polyA RNA isolated from THP-1 promonocyte cells treated for three days with 0.8 micromolar 5-aza-2'-deoxycytidine. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
158	1831477	THP1AZT01	The library was constructed using 1 microgram of polyA RNA isolated from THP-1 promonocyte cells treated for three days with 0.8 micromolar 5-aza-2'-deoxycytidine. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.
159	1841607	COLNNOT07	The library was constructed using RNA isolated from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy.
160	1852391	LUNGFET03	The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
161	1854555	HNT3AZT01	Library was constructed using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated for three days with 0.35 micromolar 5-aza-2'-deoxycytidine (AZT).
162	1855755	PROSNOT18	The library was constructed using RNA isolated from diseased prostate tissue removed from a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated adenofibromatous hyperplasia. This tissue was associated with a grade 3 transitional cell carcinoma. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
163	1861434	PROSNOT19	The library was constructed using RNA isolated from diseased prostate tissue removed from a 59-year-old Caucasian male during a radical prostatectomy with regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3+3). The patient presented with elevated prostate-specific antigen (PSA). Patient history included colon diverticuli and thrombophlebitis. Family history included benign hypertension, multiple myeloma, hyperlipidemia and rheumatoid arthritis.
164	1872334	LEUKNOT02	The library was constructed using RNA isolated from white blood cells of a 45-year-old female with blood type O+. The donor tested positive for cytomegalovirus (CMV).
165	1877230	LEUKNOT03	The library was constructed using RNA isolated from white blood cells of a 27-year-old female with blood type A+. The donor tested negative for cytomegalovirus (CMV).

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
166	1877885	LEUKNOT03	The library was constructed using RNA isolated from white blood cells of a 27-year-old female with blood type A+. The donor tested negative for cytomegalovirus (CMV).
167	1889269	BLADTUT07	The library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
168	1890243	BLADTUT07	The library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
169	1900433	BLADTUT06	The library was constructed using RNA isolated from bladder tumor tissue removed from the posterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated grade 3 transitional cell carcinoma in the left lateral bladder wall. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
170	1909441	CONNTUT01	The library was constructed using RNA isolated from a soft tissue tumor removed from the clival area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chordoma with neoplastic cells reactive for keratin.
171	1932226	COLNNOT16	The library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy.
172	1932647	COLNNOT16	The library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
173	2124245	BRSTNOT07	The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, atherosclerotic coronary artery disease, and type II diabetes.
174	2132626	OVARNOT03	The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, cerebrovascular disease, breast cancer, and uterine cancer.
175	2280639	PROSNON01	The library was constructed and normalized from 4.4 million independent clones from the PROSNON01 library. Starting RNA was made from prostate tissue removed from a 28-year-old Caucasian male who died from a gunshot wound. The normalization and hybridization conditions were adapted from Soares, M.B. et al. (1994) Proc. Natl. Acad. Sci. USA 91:9228-9232, using a longer (19 hour) reannealing hybridization period.
176	2292356	BRAINON01	The library was constructed and normalized from 4.88 million independent clones from the BRAINON01 library. Starting RNA was made from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.
177	2349310	COLSUCT01	The library was constructed using RNA isolated from diseased sigmoid colon tissue obtained from a 70-year-old Caucasian male during colectomy with permanent ileostomy. Pathology indicated chronic ulcerative colitis. Patient history included benign neoplasm of the colon. Family history included atherosclerotic coronary artery disease and myocardial infarctions.
178	2373227	ADRENOT07	The library was constructed using RNA isolated from adrenal tissue removed from a 61-year-old female during a bilateral adrenalectomy. Patient history included an unspecified disorder of the adrenal glands.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
179	2457682	ENDANOT01	The library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.
180	2480426	SMCANOT01	The library was constructed using RNA isolated from an aortic smooth muscle cell line derived from the explanted heart of a male during a heart transplant.
181	2503743	CONUTUT01	The library was constructed using RNA isolated from sigmoid mesentery tumor tissue obtained from a 61-year-old female during a total abdominal hysterectomy and bilateral salpingo-oophorectomy with regional lymph node excision. Pathology indicated a metastatic grade 4 malignant mixed müllerian tumor present in the sigmoid mesentery at two sites.
182	2537684	BONRTUT01	The library was constructed using RNA isolated from rib tumor tissue removed from a 16-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated a metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.
183	2593853	OVARTUT02	The library was constructed using RNA isolated from ovarian tumor tissue removed from a 51-year-old Caucasian female during an exploratory laparotomy, total abdominal hysterectomy, salpingo-oophorectomy, and an incidental appendectomy. Pathology indicated mucinous cystadenoma presenting as a multiloculated neoplasm involving the entire left ovary. The right ovary contained a follicular cyst and a hemorrhagic corpus luteum. The uterus showed proliferative endometrium and a single intramural leiomyoma. The peritoneal biopsy indicated benign glandular inclusions consistent with endosalpingiosis. Family history included atherosclerotic coronary artery disease, benign hypertension, breast cancer, and uterine cancer.
184	2622354	KERANOT02	The library was constructed using RNA isolated from epidermal breast keratinocytes (NHEK). NHEK (Clontech #CC-2501) is a human breast keratinocyte cell line derived from a 30-year-old black female during breast-reduction surgery.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
185	2641377	LUNGTUT08	The library was constructed using RNA isolated from lung tumor tissue removed from a 63-year-old Caucasian male during a right upper lobectomy with fiberoptic bronchoscopy. Pathology indicated a grade 3 adenocarcinoma. Patient history included atherosclerotic coronary artery disease, an acute myocardial infarction, renal cancer, an asymptomatic abdominal aortic aneurysm, and cardiac dysrhythmia. Family history included congestive heart failure, stomach cancer, and lung cancer, type II diabetes, atherosclerotic coronary artery disease, and an acute myocardial infarction.
186	2674857	KIDNNOT19	The library was constructed using RNA isolated from kidney tissue removed a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Pathology for the associated tumor tissue indicated a grade I renal cell carcinoma within the upper pole of the left kidney. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included myocardial infarction, atherosclerotic coronary artery disease, cerebrovascular disease, prostate cancer, myocardial infarction, and atherosclerotic coronary artery disease.
187	2758485	THPIAZS08	The subtracted THP-1 promonocyte cell line library was constructed using 5.76 million clones from a 5-aza-2'-deoxycytidine (AZT) treated THP-1 cell library. Starting RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZT. The library was oligo(dT)-primed, and cDNAs were cloned directionally into the pSPORT1 vectoring system using SalI (5') and NotI (3'). The hybridization probe for subtraction was derived from a similarly constructed library, made from 1 microgram of polyA RNA isolated from untreated THP-1 cells. 5.76 million clones from the AZ-treated THP-1 cell library were then subjected to two rounds of subtractive hybridization with 5 million clones from the untreated THP-1 cell library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al. (Nucl. Acids Res. (1991) 19:1954) and Bonaldo et al. (Genome Res (1996) 6: 791-806).
188	2763296	BRSTNOT12	The library was constructed using RNA isolated from diseased breast tissue removed from a 32-year-old Caucasian female during a bilateral reduction mammoplasty. Pathology indicated nonproliferative fibrocystic disease. Family history included benign hypertension and atherosclerotic coronary artery disease.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
189	2779436	OVARTUT03	The library was constructed using RNA isolated from ovarian tumor tissue removed from the left ovary of a 52-year-old mixed ethnicity female during a total abdominal hysterectomy, bilateral salpingo-oophorectomy, peritoneal and lymphatic structure biopsy, regional lymph node excision, and peritoneal tissue destruction. Pathology indicated an invasive grade 3 (of 4) seroanaplastic carcinoma forming a mass in the left ovary. The endometrium was atrophic. Multiple (2) leiomyomata were identified, one subserosal and 1 intramural. Pathology also indicated a metastatic grade 3 seroanaplastic carcinoma involving the omentum, cul-de-sac peritoneum, left broad ligament peritoneum, and mesentery colon. Patient history included breast cancer, chronic peptic ulcer, and joint pain. Family history included colon cancer, cerebrovascular disease, breast cancer, type II diabetes, esophagus cancer, and depressive disorder.
190	2808528	BLADTUT08	The library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Family history included myocardial infarction, cerebrovascular disease, brain cancer, and myocardial infarction.
191	2809230	BLADTUT08	The library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Patient history included pure hypercholesterolemia and tobacco abuse. Family history included myocardial infarction, cerebrovascular disease, brain cancer, and myocardial infarction.
192	2816821	BRSTNOT14	The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. The tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, and cardiac dysrhythmia. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
193	2817268	BRSTNOT14	The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. The tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, and cardiac dysrhythmia. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.
194	2923165	SININOT04	The library was constructed using RNA isolated from diseased ileum tissue obtained from a 26-year-old Caucasian male during a partial colectomy, permanent colostomy, and an incidental appendectomy. Pathology indicated moderately to severely active Crohn's disease. Family history included enteritis of the small intestine.
195	2949822	KIDNFET01	The library was constructed using RNA isolated from kidney tissue removed from a Caucasian female fetus, who died at 17 weeks' gestation from anencephalus.
196	2992192	KIDNFET02	The library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart and died at 23 weeks' gestation.
197	2992458	KIDNFET02	The library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart and died at 23 weeks' gestation.
198	3044710	HEAANOT01	The library was constructed using RNA isolated from right coronary and right circumflex coronary artery tissue removed from the explanted heart of a 46-year-old Caucasian male during a heart transplantation. Patient history included myocardial infarction from total occlusion of the left anterior descending coronary artery, atherosclerotic coronary artery disease, hyperlipidemia, myocardial ischemia, dilated cardiomyopathy, and left ventricular dysfunction. Previous surgeries included cardiac catheterization. Family history included atherosclerotic coronary artery disease.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
199	3120415	LUNGTUT13	The library was constructed using RNA isolated from tumorous lung tissue removed from the right upper lobe of a 47-year-old Caucasian male during a segmental lung resection. Pathology indicated invasive grade 3 (of 4) adenocarcinoma. Family history included atherosclerotic coronary artery disease, and type II diabetes.
200	126758	LUNGNOT01	The library was constructed at Stratagene using RNA isolated from the lung tissue of a 72-year-old male.
201	674760	CRBLNOT01	The library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis.
202	1229438	BRAITUT01	The library was constructed using RNA isolated from brain tumor tissue removed from a 50-year-old Caucasian female during a frontal lobectomy. Pathology indicated recurrent grade 3 oligoastrocytoma with focal necrosis and extensive calcification. Patient history included a speech disturbance and epilepsy. The patient's brain had also been irradiated with a total dose of 5,082 cGy (Fraction 8). Family history included a brain tumor.
203	1236935	LUNGFET03	The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus who died at 20 weeks' gestation.
204	1359283	LUNGNOT12	The library was constructed using RNA isolated from lung tissue removed from a 78-year-old Caucasian male during a segmental lung resection and regional lymph node resection. Pathology indicated fibrosis pleura was puckered, but not invaded. Pathology for the associated tumor tissue indicated an invasive pulmonary grade 3 adenocarcinoma. Patient history included cerebrovascular disease, arteriosclerotic coronary artery disease, thrombophlebitis, chronic obstructive pulmonary disease, and asthma. Family history included intracranial hematoma, cerebrovascular disease, arteriosclerotic coronary artery disease, and type I diabetes.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
205	1450703	PENITUT01	The library was constructed using RNA isolated from tumor tissue removed from the penis of a 64-year-old Caucasian male during penile amputation. Pathology indicated a fungating invasive grade 4 squamous cell carcinoma involving the inner wall of the foreskin and extending onto the glans penis. Patient history included benign neoplasm of the large bowel, atherosclerotic coronary artery disease, angina pectoris, gout, and obesity. Family history included malignant pharyngeal neoplasm, chronic lymphocytic leukemia, and chronic liver disease.
206	1910668	CONNTUT01	The library was constructed using RNA isolated from a soft tissue tumor removed from the clival area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chordoma with neoplastic cells reactive for keratin.
207	1955143	CONNNOT01	The library was constructed using RNA isolated from mesentery fat tissue obtained from a 71-year-old Caucasian male during a partial colectomy and permanent colostomy. Family history included atherosclerotic coronary artery disease, myocardial infarction, and extrinsic asthma.
208	1961637	BRSTNOT04	The library was constructed using RNA isolated from breast tissue removed from a 62-year-old East Indian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 ductal carcinoma. Patient history included benign hypertension, hyperlipidemia, and hematuria. Family history included cerebrovascular and cardiovascular disease, hyperlipidemia, and liver cancer.
209	1990762	CORPNOT02	The library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
210	1994131	CORPNOT02	The library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
211	1997745	BRSTTUT03	The library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multicentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type 1 diabetes.
212	2009035	TESTNOT03	The library was constructed using polyA RNA isolated from testicular tissue removed from a 37-year-old Caucasian male who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.
213	2009152	TESTNOT03	The library was constructed using polyA RNA isolated from testicular tissue removed from a 37-year-old Caucasian male who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.
214	2061752	OVARNOT03	The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
215	2061933	OVARNOT03	The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
216	2081422	UTRSNOT08	The library was constructed using RNA isolated from uterine tissue removed from a 35-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. Pathology indicated that the endometrium was secretory phase with a benign endometrial polyp 1 cm in diameter. The cervix showed mild chronic cervicitis. Family history included atherosclerotic coronary artery disease and type II diabetes.
217	2101278	BRAITUT02	The library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a grade 2 metastatic hypernephroma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.
218	2121353	BRSTNOT07	The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.
219	2241736	PANCTUT02	The library was constructed using RNA isolated from pancreatic tumor tissue removed from a 45-year-old Caucasian female during radical pancreaticoduodenectomy. Pathology indicated a grade 4 anaplastic carcinoma. Family history included benign hypertension, hyperlipidemia and atherosclerotic coronary artery disease.
220	2271935	PROSNON01	This normalized prostate library was constructed from 4.4 M independent clones from the PROSNOT11 library. Starting RNA was made from prostate tissue removed from a 28-year-old Caucasian male who died from a self-inflicted gunshot wound. The normalization and hybridization conditions were adapted from Soares, M.B. et al. (1994) Proc. Natl. Acad. Sci. USA 91:9228-9232, using a longer (19 hour) reannealing hybridization period.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
221	2295344	BRSTNOT05	The library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.
222	2303994	BRSTNOT05	The library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.
223	2497805	ADRETUT05	The library was constructed RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
224	2646362	LUNGTUT11	The library was constructed using RNA isolated from lung tumor tissue removed from the right lower lobe a 57-year-old Caucasian male during a segmental lung resection. Pathology indicated an infiltrating grade 4 squamous cell carcinoma. Multiple intrapulmonary peribronchial lymph nodes showed metastatic squamous cell carcinoma. Patient history included a benign brain neoplasm and tobacco abuse. Family history included spinal cord cancer, type II diabetes, cerebrovascular disease, and malignant prostate neoplasm.
225	2657146	LUNGTUT09	The library was constructed using RNA isolated from lung tumor tissue removed from a 68-year-old Caucasian male during segmental lung resection. Pathology indicated invasive grade 3 squamous cell carcinoma and a metastatic tumor. Patient history included type II diabetes, thyroid disorder, depressive disorder, hyperlipidemia, esophageal ulcer, and tobacco use.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
226	2755786	THPIAZS08	This subtracted THP-1 promonocyte cell line library was constructed using 5.76 million clones from a 5-aza-2'-deoxycytidine (AZ) treated THP-1 cell library. Starting RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZ. The hybridization probe for subtraction was derived from a similarly constructed library, made from RNA isolated from untreated THP-1 cells. 5.76 million clones from the AZ-treated THP-1 cell library were then subjected to two rounds of subtractive hybridization with 5 million clones from the untreated THP-1 cell library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR (1991) 19:1954, and Bonaldo et al., Genome Research (1996) 6:791. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.
227	2831245	TLVMNOT03	The library was constructed using RNA isolated from nonactivated Th1 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-12 and B7-transfected COS cells.
228	3116250	LUNGTUT13	The library was constructed using RNA isolated from tumorous lung tissue removed from the right upper lobe of a 47-year-old Caucasian male during a segmental lung resection. Pathology indicated invasive grade 3 (of 4) adenocarcinoma. Family history included atherosclerotic coronary artery disease, and type II diabetes.
229	3129630	LUNGTUT12	The library was constructed using RNA isolated from tumorous lung tissue removed from a 70-year-old Caucasian female during a lung lobectomy of the left upper lobe. Pathology indicated grade 3 (of 4) adenocarcinoma and vascular invasion. Patient history included tobacco abuse, depressive disorder, anxiety state, and skin cancer. Family history included cerebrovascular disease, congestive heart failure, colon cancer, depressive disorder, and primary liver.
230	007632	HMCINOT01	The library was constructed using RNA isolated from the HMC-1 human mast cell line derived from a 52-year-old female. Patient history included mast cell leukemia.
231	1236968	LUNGFET03	The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus who died at 20 weeks' gestation.
232	1334153	COLNNOT13	The library was constructed using RNA isolated from ascending colon tissue of a 28-year-old Caucasian male with moderate chronic ulcerative colitis.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
233	1396975	BRAITUT08	The library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 47-year-old Caucasian male during excision of cerebral meningeal tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumoral radionecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia, epilepsy, and tobacco use. Family history included cerebrovascular disease and malignant prostate neoplasm.
234	1501749	SINTBST01	The library was constructed using RNA isolated from ileum tissue removed from an 18-year-old Caucasian female during bowel anastomosis. Pathology indicated Crohn's disease of the ileum. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
235	1575240	LNODNOT03	The library was constructed using RNA isolated from lymph node tissue removed from a 67-year-old Caucasian male during a segmental lung resection and bronchoscopy. This tissue was extensively necrotic with 10% viable tumor. Pathology for the associated tumor tissue indicated invasive grade 3-4 squamous cell carcinoma. Patient history included hemangioma. Family history included atherosclerotic coronary artery disease, benign hypertension, and congestive heart failure.
236	1647884	PROSTUT09	The library was constructed using RNA isolated from prostate tumor tissue removed from a 66-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma. Patient history included lung neoplasm, and benign hypertension. Family history included malignant breast neoplasm, tuberculosis, cerebrovascular disease, atherosclerotic coronary artery disease, and lung cancer.
237	1661144	BRSTNOT09	The library was constructed using RNA isolated from breast tissue removed from a 45-year-old Caucasian female during unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated invasive nuclear grade 2-3 adenocarcinoma. Patient history included valvuloplasty of mitral valve and rheumatic heart disease. Family history included cardiovascular disease and type II diabetes.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
238	1685409	PROSNOT15	The library was constructed using RNA isolated from diseased prostate tissue removed from a 66-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated adenocarcinoma (Gleason grade 2+3). The patient presented with elevated prostate specific antigen (PSA). Family history included prostate cancer, secondary bone cancer, and benign hypertension.
239	1731419	BRSTTUT08	The library was constructed using RNA isolated from breast tumor tissue removed from a 45-year-old Caucasian female during unilateral extended simple mastectomy. Pathology indicated invasive nuclear grade 2-3 adenocarcinoma. Patient history included valvuloplasty of mitral valve and rheumatic heart disease. Family history included cardiovascular disease and type II diabetes.
240	2650265	BRSTNOT14	The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma. Patient history included a benign colon neoplasm, hyperlipidemia, cardiac dysrhythmia, and obesity. Family history included cardiovascular and cerebrovascular disease and colon, ovary and lung cancer.
241	2677129	KIDNNOT19	The library was constructed using RNA isolated from kidney tissue removed a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Pathology for the associated tumor tissue indicated grade 1 renal cell carcinoma within the upper pole of the left kidney. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included myocardial infarction, atherosclerotic coronary artery disease, cerebrovascular disease, and prostate cancer.
242	3151073	ADRENON04	The normalized adrenal gland library was constructed from 1.36 x 1e6 independent clones from an adrenal tissue library. Starting RNA was made from adrenal gland tissue removed from a 20-year-old Caucasian male who died from head trauma. The library was normalized in two rounds using conditions adapted from Soares et al. (PNAS (1994) 91:9228-9232) and Bonaldo et al. (Genome Res (1996) 6: 791-806) using a significantly longer (48-hours/round) reannealing hybridization period.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
243	3170095	BRSTNOT18	The library was constructed using RNA isolated from diseased breast tissue removed from a 57-year-old Caucasian female during a unilateral simple extended mastectomy. Pathology indicated mildly proliferative breast disease. Patient history included breast cancer and osteoarthritis. Family history included type II diabetes, gallbladder and breast cancer, and chronic lymphocytic leukemia.
244	3475168	LUNGNOT27	The library was constructed using RNA isolated from lung tissue removed from a 17-year-old Hispanic female.
245	3836893	DENDTNT01	The library was constructed using RNA isolated from treated dendritic cells from peripheral blood.
246	4072159	KIDNNOT26	The library was constructed using RNA isolated from left kidney medulla and cortex tissue removed from a 53-year-old Caucasian female during a nephroureterectomy. Pathology for the associated tumor tissue indicated grade 2 renal cell carcinoma involving the lower pole of the kidney. Patient history included hyperlipidemia, cardiac dysrhythmia, menorrhagia, cerebrovascular disease, atherosclerotic coronary artery disease, and tobacco abuse. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.
247	1003916	BRSTNOT03	The library was constructed using RNA isolated from diseased breast tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy. Pathology for the associated tumor tissue indicated residual invasive grade 3 mammary ductal adenocarcinoma. Patient history included kidney infection and condyloma acuminatum. Family history included benign hypertension, hyperlipidemia and a malignant neoplasm of the colon.
248	2093492	PANCNOT04	The library was constructed using RNA isolated from the pancreatic tissue of a 5-year-old Caucasian male who died in a motor vehicle accident.
249	2108789	BRAITUT03	The library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 17-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a grade 4 fibrillary giant and small-cell astrocytoma. Family history included benign hypertension and cerebrovascular disease.
250	2171401	ENDCNOT03	The library was constructed using RNA isolated from dermal microvascular endothelial cells removed from a neonatal Caucasian male.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
251	2212530	SINTFET03	The library was constructed using RNA isolated from small intestine tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
252	2253036	OVRTUT01	The library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
253	2280161	PROSNON01	The normalized prostate library was constructed from 4.4 M independent clones from the PROSNOT11 library. Starting RNA was made from prostate tissue removed from a 28-year-old Caucasian male who died from a self-inflicted gunshot wound. The normalization and hybridization conditions were adapted from Soares, M.B. et al. (1994) Proc. Natl. Acad. Sci. USA 91:9228-9232, using a longer (19 hour) reannealing hybridization period.
254	2287485	BRAINON01	The library was constructed and normalized from 4.88 million independent clones from the BRAINOT03 library. RNA was made from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.
255	2380344	ISLTNOT01	The library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.
256	2383171	ISLTNOT01	The library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.
257	2396046	THP1AZT01	The library was constructed using RNA isolated from THP-1 promonocyte cells treated for three days with 0.8 micromolar 5-aza-2'-deoxycytidine. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.
258	2456587	ENDANOT01	The library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
259	2484813	BONRTUT01	The library was constructed using RNA isolated from rib tumor tissue removed from a 16-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated a metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.
260	2493851	ADRETUT05	The library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
261	2495719	ADRETUT05	The library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.
262	2614153	GBLANOT01	The library was constructed using RNA isolated from diseased gallbladder tissue removed from a 53-year-old Caucasian female during a cholecystectomy. Pathology indicated mild chronic cholecystitis and cholelithiasis with approximately 150 mixed gallstones. Family history included benign hypertension.
263	2655184	THYMNOT04	The library was constructed using RNA isolated from thymus tissue removed from a 3-year-old Caucasian male, who died from anoxia. Serologies were negative. The patient was not taking any medications.
264	2848362	BRSTTUT13	The library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.
265	2849906	BRSTTUT13	The library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.

TABLE 4 (cont.)

Polynucleotide SEQ ID NO:	Clone ID	Library	Library Description
266	2899137	DRGCNOT01	The library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and steatosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell's palsy. Surgeries included colonoscopy, large intestine biopsy, adenotonsillectomy, and nasopharyngeal endoscopy and biopsy; treatment included radiation therapy.
267	2986229	CARGDIT01	The library was constructed using RNA isolated from diseased cartilage tissue. Patient history included osteoarthritis.
268	3222081	COLNNON03	The normalized colon library was constructed from 2.84×10^6 independent clones from the COLNNOT07 library. Starting RNA was made from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy. The normalization and hybridization conditions were adapted from Soares et al. (PNAS (1994) 91:9228-9232), Swaroop et al. (Nucl. Acids Res. (1991) 19:1954) and Bonaldo et al. (Genome Res (1996) 6: 791-806), using a significantly longer (48 hour) reannealing hybridization period.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLJMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, Nucl. Acid Res. 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <u>supra</u> ; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

TABLE 6

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
135	443531	443531H1	1	253
		1406807F6	152	336
		443531T6	847	355
		SBBA00451F1	396	856
		SBBA00676F1	546	865
136	632860	632860H1	13	253
		784715R3	17	666
		509590H1	455	706
137	670010	670010H1	1	263
		669971R1	1	633
138	726498	726498H1	13	263
		726498R6	13	489
		866599R3	7	660
		795064H1	86	323
139	795064	4339458H1	4	284
		937605R3	86	505
		2381151F6	592	1057
		1466346F6	857	1241
		924925H1	111	412
140	924925	3268330H1	2	239
		759120R3	111	629
		1907958F6	1	478
141	962390	023569F1	1122	470
		167282F1	1216	543
		1309211F1	911	1224

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
142	1259405	1259405H1	46	277
		2472425H1	331	354
		774303R1	190	743
		1520779F1	418	1001
		1693833F6	914	1467
143	1297384	1831858T6.comp	1336	1742
		1527737T6.comp	1386	1829
		1297384H1	402	641
		1269310F6	1	492
		1457367F1	792	1380
144	1299627	415587R1	1358	1712
		SANA02967F1	1143	614
		1299627H1	1	250
		1359140F6	1004	1573
		1349224F1	1330	1731
145	1306026	SBAA01431F1	46	397
		SBAA02909F1	868	262
		SBAA01156F1	901	1266
		1306026H1	1	223
		1464088R6	302	829
146	1316219	SBAA02496F1	92	568
		SBAA04305F1	366	883
		1316219H1	246	491
		2458603F6	1	402
		2504756T6	980	380
147	1329031	1329031H1	1	264
		1329031T6	505	1
		1329031F6	1	523

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
148	1483050	1483050H1	722	931
		855049H1	1	267
		077017F1	1069	679
		1483050F6	722	1215
		1480024T6	2063	1315
		1483050T6	2068	1535
		759486R1	1762	2089
149	1514160	1514160H1	1640	1838
		1866765T7	2383	2210
		782676R1	1652	1875
		008055X4	1090	1804
		008055X5	1316	1952
		1866765F6	2209	2391
		SAOA03127F1	2129	1703
150	1603403	1603403H1	7	224
		372910F1	420	44
		733299R7	219	420
151	1652303	1652303H1	4	256
		1671806H1	1	224
		1341743T1	2069	1900
		3803812H1	389	697
		1878546F6	747	1344
		1428640F1	1081	1664
		2058609R6	1715	2098
		1331621F1	1780	2096
		1306331T1	1897	2098

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
152	1693358	1693358H1	41	125
		2498265H1	1	252
		1867125F6	205	373
		1693358T6	1094	416
		2245848R6	737	1103
153	1707711	1707711H1	408	626
		1484609T1	2165	1855
		1707711F6	408	987
		1267959F1	1721	2182
		1484609F1	1855	2178
		SAJA00930F1	544	1132
		SAJA01300R1	1675	1212
		SAJA00999R1	1675	1142
154	1738735	1738735H1	7	236
		SAJA00944R1	393	5
		SAJA00137F1	913	685
		SAJA03629F1	435	42
155	1749147	1749147H1	1	276
155		1749147F6	47	457
155		1749147T6	479	1
156	1817722	1817722H1	1	268
		2011085H1	344	545
157	1831290	1831290H1	10	257
		3473958H1	70	242
		1972268F6	163	617
		1301277F1	413	852
		1521574F1	1024	1602
		1561690T6	1729	1058
		891461R1	1261	1738

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
158	1831477	1831477H1	59	337
		1582867H1	1	199
		1336769T1	1986	1639
		1933092H1	525	789
		1519909F1	841	1296
		1220946H1	1061	1318
		809556T1	1983	1687
159	1841607	1217559T1	2002	1445
		1309225F1	1747	2001
		1841607H1	13	192
		SBHA03588F1	13	172
		1852391H1	98	367
		734140H1	1	225
		1852391F6	98	542
161	1854555	1854555H1	1	265
		2511711H1	37	58
		782453R1	223	712
		1854555F6	1	346
		1840675T6	1046	860
		2109736H1	938	1054
		1855755H1	17	224
162	1855755	3040236H1	1	179
		1283207F1	306	816
		833763T1	1148	835
		1920926R6	854	1161
		1861434H1	13	253
		1861434T6	872	261
		SARA01525F1	426	808
163	1861434	SARA02548F1	587	889

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
164	1872334	1872334HI	1	229
		1872334F6	1	424
		SBGA03684F1	358	425
165	1877230	1877230HI	1405	1677
		2519841HI	1	251
		1877230T6	1903	1405
		1254693F1	335	716
		077020R1	682	1414
		1232336F1	906	1507
		1004952R6	1451	1904
		SARA01879F1	1545	1921
		SARA02654F1	1545	1923
166	1877885	1877885HI	68	323
		508020F1	499	51
		2751126R6	219	516
		SARA02571F1	407	499
167	1889269	1889269HI	757	1020
		1915551HI	1	191
		629493X12	481	865
		1441289F1	693	865
		1215274X34F1	1106	1631
		1818447F6	1307	1540
		1208463R1	1372	1493
168	1890243	1890243HI	9	268
		SARA01884F1	521	168
		SATA00046F1	1057	851
		SARA03294F1	1329	910
		SARA02790F1	1138	1535

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
169	1900433	1900433HI SATA00396FI SATA02742FI	1 409 1	242 124 294
170	1909441	1909441HI 1398811FI 3039939HI 3324740HI 1442131F6 2254056HI 2199453T6 1698531HI	786 1 607 685 787 1423 1955 1968	1048 550 876 944 1232 1522 1351 1796
171	1932226	1932226HI 2320569HI 1932226F6 2469455T6 2469455F6 1907140F6 SATA02592FI	294 1 294 1475 1034 1158 857	510 266 685 1071 1492 1482 518
172	1932647	1932647HI 1492745T1 1492745HI SASA02355FI SASA00117FI SASA00192FI	17 1582 1418 386 250 515	246 1418 1599 19 569 816
173	2124245	2124245HI 1235393FI 1402264F6 1303990FI 1402264T6	45 495 323 682 1613	190 895 925 1240 950

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
174	2132626	2132626H1	406	651
		1723432T6	1299	746
		2132626R6	406	904
		1736723T6	1292	857
		1504738F1	868	1320
175	2280639	2280639H1	28	303
		1377560F6	261	777
176	2292356	2292356H1	717	968
		4086827H1	1	275
		1754442F6	232	577
		3571126H1	497	808
		1601305F6	808	1464
177	2349310	2349310H1	1	236
		2349310T6	682	2
178	2373227	2373227H1	298	524
		3316444H1	801	1053
		302685R6	1141	1496
		SASA02181F1	577	1
		SASA01923F1	963	466
		SASA03516F1	1102	1249
179	2457682	2457682H1	1	226
		2457682F6	1	554
180	2480426	2480426H1	1	213
		2480426F6	1	501

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
181	2503743	2503743HI	6	222
		1853909HI	1	272
		1517619F1	172	830
		1467896F6	540	1112
		490031F1	1647	1068
182	2537684	1208654R1	1382	1633
		880544R1	1450	1648
		2537684HI	434	682
		2005493HI	1	194
		730969HI	307	547
183	2593853	916487HI	723	989
		996135R1	997	1598
		1920738R6	1306	1692
		1957710F6	1472	1692
		2593853HI	1	252
184	2622354	807497HI	2	217
		914020R6	284	740
		889992R1	416	729
		2622354HI	3	266
		2623992HI	1	246
185	2641377	1556510F6	81	258
		2641377HI	126	369
		4341415H2	10	345
		SBCA07049F3	126	599

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
186	2674857	2674857H1	139	393
		1872373H1	1	270
		470512R6	1486	1502
		1728547H1	1285	1508
		3013651F6	1423	1987
		SBCA01366F1	819	385
187	2758485	SBCA00694F1	973	1198
		2758485H1	20	267
		3097533H1	1	158
		1578959F6	291	771
		2763296H1	63	301
		3486025F6	1	130
188	2763296	SBDA07002F3	63	687
		2779436H1	1	233
		2779436F6	1	577
		SBDA07009F3	1	608
		2808528H1	25	335
		2611513F6	2	489
189	2779436	SBDA07021T3	1058	443
		2809230H1	409	630
		2213849H1	1	133
		711706R6	396	691
		958323R1	407	800
		030732F1	1366	623
190	2808528	2816821H1	210	501
		3746964H1	1	307
		2816821F6	210	682
		948722T6	959	527
		2809230		
		2816821		
191	2809230			
192	2816821			

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
193	2817268	2817268H1	42	282
		3591308H1	13	264
		419522R1	179	808
		2073028F6	446	924
		1308781F6	869	1112
194	2923165	2923165H1	8	295
		2011630H1	18	238
		1457250F1	268	856
		754668R1	327	878
		1406510F6	558	901
195	2949822	2949822H1	1	280
		SBDA07078F3	1	606
196	2992192	2992192H1	25	321
		2534324H2	1	240
		2815255T6	690	219
		1551107T6	893	471
		1551107R6	471	690
197	2992458	2992458H1	48	362
		2618951H1	1	247
		1479252F1	163	610
		1879054H1	563	840
		1879054F6	563	1096
		2215240H1	951	1202
		1535968T1	1729	1173

TABLE 6 (cont.)

Nucleotide SEQ ID NO:	Clone ID	Fragment of SEQ ID NO	Starting Nucleotide of Fragment	Ending Nucleotide of Fragment
198	3044710	3044710H1	652	952
		3741773H1	1	283
		859906X42C1	94	192
		1534347F1	90	268
		1421122F1	830	1392
		1303865F1	1033	1487
		1704452F6	1432	1934
		1251642F1	2006	1544
		1781694R6	1894	2017
199	3120415	3120415H1	72	363
		1360123T1	523	141
		1375015H1	380	526

What is claimed is:

1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134 (SEQ ID NO:1-134), and fragments thereof.

2. A substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of claim 1.

3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
4. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 3.
- 5 5. An isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
7. A method for detecting a polynucleotide, the method comprising the steps
10 of:
 - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the
15 sample.
8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
9. An isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:135, SEQ ID NO:136, SEQ
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10. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 9.

11. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 9.

12. An expression vector comprising at least a fragment of the polynucleotide of claim 3.

13. A host cell comprising the expression vector of claim 12.

14. A method for producing a polypeptide, the method comprising the steps of:
a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and

b) recovering the polypeptide from the host cell culture.

15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.

16. A purified antibody which specifically binds to the polypeptide of claim 1.

17. A purified agonist of the polypeptide of claim 1.

18. A purified antagonist of the polypeptide of claim 1.

19. A method for treating or preventing a disorder associated with decreased expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 15.

20. A method for treating or preventing a disorder associated with increased
5 expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 18.

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.

LAL, Preeti
 TANG, Y. Tom
 GORGONE, Gina A.
 CORLEY, Neil C.
 GUEGLER, Karl J.
 BAUGHN, Mariah R.
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 AU-YOUNG, Janice
 YUE, Henry
 PATTERSON, Chandra
 REDDY, Roopa
 HILLMAN, Jennifer L.
 BANDMAN, Olga

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<140> To Be Assigned

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<151> 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11

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				20					25					30
Gln	His	Asp	Gly	Ala	Gln	Pro	Ser	Pro	Lys	Cys	Leu	Ala	Glu	Glu
				35					40					45
Leu	Gly	Asp	Ala	Trp	Thr	Ile	Gln	Ile	Glu	Ala	Asn	Trp	Lys	Tyr
				50					55					60
Arg	Ala	Val	Asn	Thr	Asn	Gln	Arg	Gly	Lys	Leu	Leu	Ala	Ser	Glu
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 35 40 45
 Phe Thr Leu Leu Asp Ser Leu Gly Leu Arg Ala Ala Gln Asp Ser
 50 55 60
 Cys Ser Phe Thr Thr Leu Val Pro Leu Thr Leu Asp Ser Ser Phe
 65 70 75
 Met Thr Val Asn Val Val Pro Phe Val Trp Thr Ser Ser Phe Phe
 80 85 90
 Arg Ala Phe Gln Tyr Pro Val Thr Ser Pro Cys Arg Thr Lys Asn
 95 100 105
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 Phe Arg Cys Arg Val Ser Val Ala Arg Glu His Leu Pro Ser Arg
 35 40 45
 Gly Ser Leu Leu Arg Gly Pro Arg Pro Arg Ile Pro Val Leu Val
 50 55 60
 Ser Cys Gln Pro Val Lys Gly His Gly Thr Leu Gly Glu Ser Pro
 65 70 75
 Met Pro Phe Lys Arg Val Phe Cys Gln Asp Gly Asn Val Arg Ser
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 35 40 45
 His Gly Arg Gln Ala Arg Ala Cys Glu Asn Leu Arg Asn Gln Thr
 50 55 60
 Arg Val Ala Thr Lys Val Glu Pro Gln Lys Gly Arg Ser Thr Glu
 65 70 75
 Ile Cys Cys Leu Ala Val Val Pro Leu Asn Glu Val Val Gln Ser
 80 85 90
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 Cys Phe Gly

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 35 40 45
 Ile Val Phe Gly Gly Gln Lys Lys Ala Thr Phe Arg Tyr His Phe
 50 55 60
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 35 40 45
 Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu
 50 55 60
 Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His
 65 70 75
 Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His
 80 85 90
 Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln
 95 100 105
 Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln
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 Glu Tyr Ala Trp Met
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 35 40 45
 Tyr Cys Cys Ser Tyr Tyr Ala Tyr Ile Gly Asn Ile Leu Ser Gly
 50 55 60
 Thr Ala Ile Ala Gly Ile Val Phe Gly Ile Val Phe Ile Met Gly
 65 70 75
 Val Ile Ala Gly Ile Ala Ile Cys Ile Cys Met Cys Met Lys Asn
 80 85 90
 His Arg Ala Thr Arg Val Gly Ile Leu Arg Thr Thr His Ile Asn
 95 100 105
 Thr Val Ser Ser Tyr Pro Gly Pro Pro Pro Tyr Gly His Asp His
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 Pro Gln Gly Pro Ala Gln Arg Ser Pro Pro Pro Pro Tyr Pro Gly
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 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser
 50 55 60
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys
 65 70 75
 Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu
 80 85 90
 Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly
 95 100 105
 Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro
 110 115 120
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 125 130 135
 Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu
 140 145 150
 Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val
 155 160 165
 Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro
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 Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu
 185 190 195
 Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys
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Asp Leu Lys Trp Asn Leu Ala Val Ile Gln Leu Phe Ser Ala Glu
      35              40              45
Gly Met Asp Thr Phe Ile Arg Val Leu Gln Lys Leu Asn Ser Ile
      50              55              60
Leu Thr Gln Pro Trp Arg Leu His Val Asn Met Gly Thr Thr Leu
      65              70              75
His Arg Val Thr Thr Ile Ser Met Ala Arg Cys Thr Leu Thr Leu
      80              85              90
Leu Lys Thr Met Leu Thr Glu Leu Leu Arg Gly Gly Ser Phe Glu
      95              100             105
Phe Lys Asp Met Arg Val Pro Ser Ala Leu Val Thr Leu His Met
      110             115             120
Leu Leu Cys Ser Ile Pro Leu Ser Gly Arg Leu Asp Ser Asp Glu
      125             130             135
Gln Lys Ile Gln Asn Asp Ile Ile Asp Ile Leu Leu Thr Phe Thr
      140             145             150
Gln Gly Val Asn Glu Lys Leu Thr Ile Ser Glu Glu Thr Leu Ala
      155             160             165
Asn Asn Thr Trp Ser Leu Met Leu Lys Glu Val Leu Ser Ser Ile
      170             175             180
Leu Lys Val Pro Glu Gly Phe Phe Ser Gly Leu Ile Leu Leu Ser
      185             190             195
Glu Leu Leu Pro Leu Pro Leu Pro Met Gln Thr Thr Gln Val Ser
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Leu Pro Tyr Asn Met His Leu Ile Asn Asp Cys Ser Asn Thr Phe
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      35              40              45
Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu
      50              55              60
Asp Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg
      65              70              75
Phe Asn Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln
      80              85              90
Tyr Gln Gln His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile

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35 40 45		
Leu Asn Lys Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp		
50 55 60		
Glu Lys Thr Tyr Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val		
65 70 75		
Gly Leu Trp Arg Arg Cys Ile Thr Ile Pro Lys Asn Met His Trp		
80 85 90		
Tyr Ser Pro Pro Glu Arg Thr Glu Ser Phe Asp Val Val Thr Lys		
95 100 105		
Cys Val Ser Phe Thr Leu Thr Glu Gln Phe Met Glu Lys Phe Val		
110 115 120		
Asp Pro Gly Asn His Asn Ser Gly Ile Asp Leu Leu Arg Thr Tyr		
125 130 135		
Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val Ser Leu Gly Leu		
140 145 150		
Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys Ile Cys Arg		
155 160 165		
Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu Leu Ala		
170 175 180		
Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly Ile		
185 190 195		
Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val Ser Gly		
200 205 210		
Glu Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro Leu		
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          20          25          30
Ser Gln Cys Cys Gln Cys Pro Trp Glu Gly Arg Ala Ser Leu Arg
          35          40          45
His Pro Asn Gly Pro Ser Gly Cys Arg Glu Ala Glu Ala Trp Pro
          50          55          60
Gln Arg Ser Leu Leu Arg Gln Gln Leu Gln Gln Ala His Pro Leu
          65          70          75
Pro Thr Leu Pro Thr Pro Glu Arg Leu Pro Glu Gln Met Leu Phe
          80          85          90
Pro Ser Ser Ser Ser Lys Pro Phe Ser Leu Leu Ser Leu Thr Ile
          95          100          105
Trp Ala Arg Leu Val Gly Arg Leu Thr Asn Arg Ile Cys Pro Val
          110          115          120
Pro Pro Gly Ser Val Ala Ser Ser Met Ser Leu Gln Ala Gly Arg
          125          130          135
Cys Gly Asn Pro Val Val Leu Pro Gln Pro Met Pro Pro Gly Leu
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Leu Cys Met Asn Glu Cys Ser Leu Val Pro Gly Leu Gly Arg Gly
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Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu
          35          40          45
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
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Cys Asn Thr

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 35 40 45
 Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
 50 55 60
 Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
 65 70 75
 Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
 80 85 90
 Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 19
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1707711

<400> 19
 Met Lys Ala Gln Pro Leu Glu Ala Leu Leu Leu Val Ala Leu Val
 1 5 10 15
 Leu Ser Phe Cys Gly Val Trp Phe Glu Asp Trp Leu Ser Lys Trp
 20 25 30
 Arg Phe Gln Cys Ile Phe Gln Leu Ala His Gln Pro Ala Leu Val
 35 40 45
 Asn Ile Gln Phe Arg Gly Thr Val Leu Gly Ser Glu Thr Phe Leu
 50 55 60
 Gly Ala Glu Glu Asn Ser Ala Asp Val Arg Ser Trp Gln Thr Leu
 65 70 75
 Ser Tyr Phe Glu Leu
 80

<210> 20
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1738735

<400> 20
 Met Ile Asp Leu Trp Leu Pro Ala Leu Phe Val Leu Val Ala Leu
 1 5 10 15
 Glu Ser Leu Leu Leu Ser Pro Cys Pro Gly Thr Ser Ser Thr Leu
 20 25 30
 Thr Arg Thr Phe Phe Pro Ser Leu Val Ser Cys Val Gln Val Pro
 35 40 45
 Phe Ser Trp Ile Pro Cys Leu Glu Cys Phe Leu Ile Tyr Phe Leu
 50 55 60
 Ile Leu Ala Glu Asp Val Leu Gln Leu Phe Ser Gly Asn Ala Asn
 65 70 75
 Met Gln Val Asn Gln

80

<210> 21

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1749147

<400> 21

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Met Gln Arg Pro Phe Leu Ser Val Pro Cys Leu Leu Leu Leu Pro
 1          5          10          15
Ala Arg Val Val Trp Gly Cys Trp Cys Phe Leu Pro Gly Glu Asp
          20          25          30
Gly Gly Gly Cys Pro Thr Pro Ser Ser Gly Arg Ile Lys Leu Leu
          35          40          45
Gln Gln Cys Leu Leu His Pro Ser Leu Arg Ser Ile Thr Val Ser
          50          55          60
Arg Arg Ser Ala Gln Leu Leu Cys Arg Leu Lys Leu Gln Asn His
          65          70          75
Ile Pro Lys Val Pro Gly Lys Asn Val
          80

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<210> 22

<211> 171

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1817722

<400> 22

```

Met His Met Ile Leu Lys Val Leu Thr Thr Ala Leu Leu Leu Gln
 1          5          10          15
Ala Ala Ser Ala Leu Ala Asn Tyr Ile His Phe Ser Ser Tyr Ser
          20          25          30
Lys Asp Gly Ile Gly Val Pro Phe Met Gly Ser Leu Ala Glu Phe
          35          40          45
Phe Asp Ile Ala Ser Gln Ile Gln Met Leu Tyr Leu Leu Leu Ser
          50          55          60
Leu Cys Met Gly Trp Thr Ile Val Arg Met Lys Lys Ser Gln Ser
          65          70          75
Arg Pro Leu Gln Trp Asp Ser Thr Pro Ala Ser Thr Gly Ile Ala
          80          85          90
Val Phe Ile Val Met Thr Gln Ser Val Leu Leu Trp Glu Gln
          95          100          105
Phe Glu Asp Ile Ser His His Ser Tyr His Ser His His Asn Leu
          110          115          120

```

Ala Gly Ile Leu Leu Ile Val Leu Arg Ile Cys Leu Ala Leu Ser
 125 130 135
 Leu Gly Cys Gly Leu Tyr Gln Ile Ile Thr Val Glu Arg Ser Thr
 140 145 150
 Leu Lys Arg Glu Phe Tyr Ile Thr Phe Ala Lys Val Trp Val Trp
 155 160 165
 Lys Glu Asn Gly Leu Phe
 170

<210> 23
 <211> 243
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1831290

<400> 23
 Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu
 1 5 10 15
 Val Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg
 20 25 30
 Pro Gly Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu
 35 40 45
 Arg Glu Asp Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu
 50 55 60
 Val Gly Gln Ala Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr
 65 70 75
 Arg Lys Asp Lys Leu Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro
 80 85 90
 Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys Gly Ser Arg His Gly
 95 100 105
 Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met Glu Tyr Tyr Asn
 110 115 120
 Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp Ala Asn Ser
 125 130 135
 Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu Thr Gly
 140 145 150
 Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu Ser
 155 160 165
 Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro
 170 175 180
 Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp Tyr Gln Asn
 185 190 195
 Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly
 200 205 210
 Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp
 215 220 225
 Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala
 230 235 240
 Thr Glu Ala

<210> 24
 <211> 311
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1831477

<400> 24
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly
 1 5 10 15
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu
 140 145 150
 Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
 155 160 165
 Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
 170 175 180
 Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala
 185 190 195
 Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
 200 205 210
 Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
 215 220 225
 Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
 230 235 240
 Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
 245 250 255
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
 260 265 270
 Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro
 275 280 285
 Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
 290 295 300
 Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
 305 310

<210> 25
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1841607

<400> 25
Met Ala Ser Ser Cys Phe Ser Leu Ser Phe Pro Pro Leu Ser Leu
1 5 10 15
Ala Gly Ser Leu Ala Leu Trp Gly His Cys Cys Val Arg Leu Gly
20 25 30
Cys Ser Phe Trp Ser Val Ser Ala Met Ala Gln Arg Leu Pro Ser
35 40 45
Gln Asn Thr Tyr Asn Pro Pro Leu Cys Trp Ala Trp
50 55

<210> 26
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1852391

<400> 26
Met Phe Ser Leu Phe Ser Cys Leu Leu Ala Cys Leu Leu Asp Leu
1 5 10 15
Leu Leu Ser Arg Val Ala Asp Glu Ala Phe Tyr Lys Gln Pro Phe
20 25 30
Ala Asp Val Ile Gly Tyr Val Tyr Val Ala Lys Leu Ile Pro Phe
35 40 45
Ser Thr Ser Asp Ser Phe Tyr Phe Cys Leu Glu Leu Met Leu Leu
50 55 60
Leu Cys His Gln Leu Leu Cys Phe Leu Asn Tyr Phe Lys Leu Ala
65 70 75
Leu Trp Gly Leu Pro Lys Asn
80

<210> 27
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1854555

<400> 27

```

Met Ala Gly Thr Val Leu Gly Val Gly Ala Gly Val Phe Ile Leu
 1          5          10          15
Ala Leu Leu Trp Val Ala Val Leu Leu Leu Cys Val Leu Leu Ser
          20          25          30
Arg Ala Ser Gly Ala Ala Arg Phe Ser Val Ile Phe Leu Phe Phe
          35          40          45
Gly Ala Val Ile Ile Thr Ser Val Leu Leu Leu Phe Pro Arg Ala
          50          55          60
Gly Glu Phe Pro Ala Pro Glu Val Glu Val Lys Ile Val Asp Asp
          65          70          75
Phe Phe Ile Gly Arg Tyr Val Leu Leu Ala Phe Leu Ser Ala Ile
          80          85          90
Phe Leu Gly Gly Leu Phe Leu Val Leu Ile His Tyr Val Leu Glu
          95          100          105
Pro Ile Tyr Ala Lys Pro Leu His Ser Tyr
          110          115

```

<210> 28

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1855755

<400> 28

```

Met Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly
 1          5          10          15
Phe Leu Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr
          20          25          30
Glu Pro Leu Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys
          35          40          45
Thr Tyr Ser Thr Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser
          50          55          60
Phe Val Gln Pro Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu
          65          70          75
Tyr Phe Thr Asn Gly His Leu Tyr Pro Thr Gly Ser Lys Ser Lys
          80          85          90
Arg Val Ser Leu Leu Gln Asn Pro Pro Thr Val Gly Val Ala Thr
          95          100          105
Leu Lys Leu Thr Asp Val His Pro Ser Asp Thr Gly Thr Tyr Leu
          110          115          120
Cys Gln Val Asn Asn Pro Pro Asp Phe Tyr Thr Asn Gly Leu Gly
          125          130          135
Leu Ile Asn Leu Thr Val Leu Val Pro Pro Ser Asn Pro Leu Cys
          140          145          150
Ser Gln Ser Gly Gln Thr Ser Val Gly Gly Ser Thr Ala Leu Arg
          155          160          165
Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val Tyr Asn Trp Val
          170          175          180
Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser Met Val Gln
          185          190          195

```

Asp	Glu	Val	Ser	Gly	Gln	Leu	Ile	Leu	Thr	Asn	Leu	Ser	Leu	Thr
				200					205					210
Ser	Ser	Gly	Thr	Tyr	Arg	Cys	Val	Ala	Thr	Asn	Gln	Met	Gly	Ser
				215					220					225
Ala	Ser	Cys	Glu	Leu	Thr	Leu	Ser	Val	Thr	Glu	Pro	Ser	Gln	Gly
				230					235					240
Arg	Val	Ala	Gly	Ala	Leu	Ile	Gly	Val	Leu	Leu	Gly	Val	Leu	Leu
				245					250					255
Leu	Ser	Val	Ala	Ala	Phe	Cys	Leu	Val	Arg	Phe	Gln	Lys	Glu	Arg
				260					265					270
Gly	Lys	Lys	Pro	Lys	Glu	Thr	Tyr	Gly	Gly	Ser	Asp	Leu	Arg	Glu
				275					280					285
Asp	Ala	Ile	Ala	Pro	Gly	Ile	Ser	Glu	His	Thr	Cys	Met	Arg	Ala
				290					295					300
Asp	Ser	Ser	Lys	Gly	Phe	Leu	Glu	Arg	Pro	Ser	Ser	Ala	Ser	Thr
				305					310					315
Val	Thr	Thr	Thr	Lys	Ser	Lys	Leu	Pro	Met	Val	Val			
				320					325					

<210> 29

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1861434

<400> 29

Met	Arg	Met	Ser	Leu	Ala	Gln	Arg	Val	Leu	Leu	Thr	Trp	Leu	Phe
1				5					10					15
Thr	Leu	Leu	Phe	Leu	Ile	Met	Leu	Val	Leu	Lys	Leu	Asp	Glu	Lys
				20					25					30
Ala	Pro	Trp	Asn	Trp	Phe	Leu	Ile	Phe	Ile	Pro	Val	Trp	Ile	Phe
				35					40					45
Asp	Thr	Ile	Leu	Leu	Val	Leu	Leu	Ile	Val	Lys	Met	Ala	Gly	Arg
				50					55					60
Cys	Lys	Ser	Gly	Phe	Asp	Pro	Arg	His	Gly	Ser	His	Asn	Ile	Lys
				65					70					75
Lys	Lys	Ala	Trp	Tyr	Leu	Ile	Ala	Met	Leu	Leu	Lys	Leu	Ala	Phe
				80					85					90
Cys	Leu	Ala	Leu	Cys	Ala	Lys	Leu	Glu	Gln	Phe	Thr	Thr	Met	Asn
				95					100					105
Leu	Ser	Tyr	Val	Phe	Ile	Pro	Leu	Trp	Ala	Leu	Leu	Ala	Gly	Ala
				110					115					120
Leu	Thr	Glu	Leu	Gly	Tyr	Asn	Val	Phe	Phe	Val	Arg	Asp		
				125					130					

<210> 30

<211> 129

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1872334

<400> 30

```

Met Gly Leu Thr Leu Leu Leu Leu Leu Leu Gly Leu Glu Gly
 1.          5          10          15
Gln Gly Ile Val Gly Ser Leu Pro Glu Val Leu Gln Ala Pro Val
          20          25          30
Gly Ser Ser Ile Leu Val Gln Cys His Tyr Arg Leu Gln Asp Val
          35          40          45
Lys Ala Gln Lys Val Trp Cys Arg Phe Leu Pro Glu Gly Cys Gln
          50          55          60
Pro Leu Val Ser Ser Ala Val Asp Arg Arg Ala Pro Ala Gly Arg
          65          70          75
Arg Thr Phe Leu Thr Asp Leu Gly Gly Gly Leu Leu Gln Val Glu
          80          85          90
Met Val Thr Leu Gln Glu Glu Asp Ala Gly Glu Tyr Gly Cys Met
          95          100          105
Val Asp Gly Ala Arg Gly Pro Gln Ile Leu His Arg Val Ser Leu
          110          115          120
Asn Ile Leu Pro Pro Gly Glu Leu Ser
          125

```

<210> 31

<211> 472

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1877230

<400> 31

```

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu
 1.          5          10          15
Ser Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys
          20          25          30
Arg Thr Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp
          35          40          45
Val Ala Lys Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln
          50          55          60
Asn Arg Ser Tyr Glu Arg Leu Ala Leu Leu Val Asp Thr Val Gly
          65          70          75
Pro Arg Leu Ser Gly Ser Lys Asn Leu Glu Lys Ala Ile Gln Ile
          80          85          90
Met Tyr Gln Asn Leu Gln Gln Asp Gly Leu Glu Lys Val His Leu
          95          100          105
Glu Pro Val Arg Ile Pro His Trp Glu Arg Gly Glu Glu Ser Ala
          110          115          120
Val Met Leu Glu Pro Arg Ile His Lys Ile Ala Ile Leu Gly Leu
          125          130          135

```

Gly Ser Ser Ile	Gly Thr Pro Pro Glu	Gly Ile Thr Ala Glu Val	
140	145	150	
Leu Val Val Thr	Ser Phe Asp Glu Leu	Gln Arg Arg Ala Ser Glu	
155	160	165	
Ala Arg Gly Lys	Ile Val Val Tyr Asn	Gln Pro Tyr Ile Asn Tyr	
170	175	180	
Ser Arg Thr Val	Gln Tyr Arg Thr Gln	Gly Ala Val Glu Ala Ala	
185	190	195	
Lys Val Gly Ala	Leu Ala Ser Leu Ile	Arg Ser Val Ala Ser Phe	
200	205	210	
Ser Ile Tyr Ser	Pro His Thr Gly Ile	Gln Glu Tyr Gln Asp Gly	
215	220	225	
Val Pro Lys Ile	Pro Thr Ala Cys Ile	Thr Val Glu Asp Ala Glu	
230	235	240	
Met Met Ser Arg	Met Ala Ser His Gly	Ile Lys Ile Val Ile Gln	
245	250	255	
Leu Lys Met Gly	Ala Lys Thr Tyr Pro	Asp Thr Asp Ser Phe Asn	
260	265	270	
Thr Val Ala Glu	Ile Thr Gly Ser Lys	Tyr Pro Glu Gln Val Val	
275	280	285	
Leu Val Ser Gly	His Leu Asp Ser Trp	Asp Val Gly Gln Gly Ala	
290	295	300	
Met Asp Asp Gly	Gly Gly Ala Phe Ile	Ser Trp Glu Ala Leu Ser	
305	310	315	
Leu Ile Lys Asp	Leu Gly Leu Arg Pro	Lys Arg Thr Leu Arg Leu	
320	325	330	
Val Leu Trp Thr	Ala Glu Glu Gln Gly	Gly Val Gly Ala Phe Gln	
335	340	345	
Tyr Tyr Gln Leu	His Lys Val Asn Ile	Ser Asn Tyr Ser Leu Val	
350	355	360	
Met Glu Ser Asp	Ala Gly Thr Phe Leu	Pro Thr Gly Leu Gln Phe	
365	370	375	
Thr Gly Ser Glu	Lys Ala Arg Ala Ile	Met Glu Glu Val Met Ser	
380	385	390	
Leu Leu Gln Pro	Leu Asn Ile Thr Gln	Val Leu Ser His Gly Glu	
395	400	405	
Gly Thr Asp Ile	Asn Phe Trp Ile Gln	Ala Gly Val Pro Gly Ala	
410	415	420	
Ser Leu Leu Asp	Asp Leu Tyr Lys Tyr	Phe Phe Phe His His Ser	
425	430	435	
His Gly Asp Thr	Met Thr Val Met Asp	Pro Lys Gln Met Asn Val	
440	445	450	
Ala Ala Ala Val	Trp Ala Val Val Ser	Tyr Val Val Ala Asp Met	
455	460	465	
Glu Glu Met Leu	Pro Arg Ser		
470			

<210> 32

<211> 93

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1877885

<400> 32

Met	Ile	His	Leu	Gly	His	Ile	Leu	Phe	Leu	Leu	Leu	Leu	Pro	Val
1				5				10					15	
Ala	Ala	Ala	Gln	Thr	Thr	Pro	Gly	Glu	Arg	Ser	Ser	Leu	Pro	Ala
				20				25					30	
Phe	Tyr	Pro	Gly	Thr	Ser	Gly	Ser	Cys	Ser	Gly	Cys	Gly	Ser	Leu
				35				40					45	
Ser	Leu	Pro	Leu	Leu	Ala	Gly	Leu	Val	Ala	Ala	Asp	Ala	Val	Ala
				50				55					60	
Ser	Leu	Leu	Ile	Val	Gly	Ala	Val	Phe	Leu	Cys	Ala	Arg	Pro	Arg
				65				70					75	
Arg	Ser	Pro	Ala	Gln	Glu	Asp	Gly	Lys	Val	Tyr	Ile	Asn	Met	Pro
				80				85					90	

Gly Arg Gly

<210> 33

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1889269

<400> 33

Met	Asn	Arg	Pro	Ser	Ala	Arg	Asn	Ala	Leu	Gly	Asn	Val	Phe	Val
1				5				10					15	
Ser	Glu	Leu	Leu	Glu	Thr	Leu	Ala	Gln	Leu	Arg	Glu	Asp	Arg	Gln
				20				25					30	
Val	Arg	Val	Leu	Leu	Phe	Arg	Ser	Gly	Val	Lys	Gly	Val	Phe	Cys
				35				40					45	
Ala	Gly	Ala	Asp	Leu	Lys	Glu	Arg	Glu	Gln	Met	Ser	Glu	Ala	Glu
				50				55					60	
Val	Gly	Val	Phe	Val	Gln	Arg	Leu	Arg	Gly	Leu	Met	Asn	Asp	Ile
				65				70					75	
Gly	Glu	Asp	Leu	Gly	Val	Gly	Trp	Arg	Arg	Gly	Phe	Gly	Gly	Pro
				80				85					90	

Cys Arg

<210> 34

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1890243

<400> 34

```

Met Trp Ile Lys Gly Thr Met Lys Met Arg Gly Gly Lys Thr Ser
 1          5          10          15
Arg Ser Ala Val Leu Pro Val Ala Gln Leu Thr Leu Ile Ala Ser
          20          25          30
Cys Phe Pro Asn Ser Gln Thr Val Leu Gly Thr Glu Gly Thr Leu
          35          40          45
Asp Val Glu Ser Ser Pro Leu Ala Leu Leu Thr Gly Leu Trp Ala
          50          55          60
Ser Pro Glu Ser Leu Ser Leu Tyr Leu Val Thr Leu Leu Cys Val
          65          70          75
Cys Pro Ala Leu Gln Ser Cys Gln Gly Gln Gln Ala Asp Val Thr
          80          85          90
Leu Ala Pro Cys Glu Ile Phe Ile Pro Gln Thr Leu Ala Cys Glu
          95          100          105
Pro Phe Pro Ser Gln Trp Arg Ala Leu Lys Gly Ala Ser Leu Glu
          110          115          120
Ser Ser Ser Val Leu Trp Val Ala Pro Cys Arg Trp Pro Leu Thr
          125          130          135
Leu Arg Cys Ser Arg Val His Leu
          140

```

<210> 35

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1900433

<400> 35

```

Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr
 1          5          10          15
Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
          20          25          30
Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
          35          40          45
Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
          50          55          60
Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
          65          70          75
Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
          80          85

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<210> 36

<211> 560

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1909441

<400> 36

Met	Ala	Lys	Lys	Lys	Leu	Thr	Glu	Met	Ile	Pro	Leu	Cys	Asn	His
1				5					10					15
Pro	Ala	Ser	Phe	Val	Lys	Leu	Phe	Val	Ala	Leu	Gly	Pro	Ile	Ala
				20					25					30
Gly	Pro	Glu	Glu	Lys	Lys	Gln	Leu	Lys	Ser	Thr	Met	Leu	Leu	Met
				35					40					45
Ser	Glu	Asp	Leu	Thr	Gly	Glu	Gln	Ala	Leu	Ala	Val	Leu	Gly	Ala
				50					55					60
Met	Gly	Asp	Met	Glu	Ser	Arg	Asn	Ser	Cys	Leu	Ile	Lys	Arg	Val
				65					70					75
Thr	Ser	Val	Leu	His	Lys	His	Leu	Asp	Gly	Tyr	Lys	Pro	Leu	Glu
				80					85					90
Leu	Leu	Lys	Ile	Thr	Gln	Glu	Leu	Thr	Phe	Leu	His	Phe	Gln	Arg
				95					100					105
Lys	Glu	Phe	Phe	Ala	Lys	Leu	Arg	Glu	Leu	Leu	Leu	Ser	Tyr	Leu
				110					115					120
Lys	Asn	Ser	Phe	Ile	Pro	Thr	Glu	Val	Ser	Val	Leu	Val	Arg	Ala
				125					130					135
Ile	Ser	Leu	Leu	Pro	Ser	Pro	His	Leu	Asp	Glu	Val	Gly	Ile	Ser
				140					145					150
Arg	Ile	Glu	Ala	Val	Leu	Pro	Gln	Cys	Asp	Leu	Asn	Asn	Leu	Ser
				155					160					165
Ser	Phe	Ala	Thr	Ser	Val	Leu	Arg	Trp	Ile	Gln	His	Asp	His	Met
				170					175					180
Tyr	Leu	Asp	Asn	Met	Thr	Ala	Lys	Gln	Leu	Lys	Leu	Leu	Gln	Lys
				185					190					195
Leu	Asp	His	Tyr	Gly	Arg	Gln	Arg	Leu	Gln	His	Ser	Asn	Ser	Leu
				200					205					210
Asp	Leu	Leu	Arg	Lys	Glu	Leu	Lys	Ser	Leu	Lys	Gly	Asn	Thr	Phe
				215					220					225
Pro	Glu	Ser	Leu	Leu	Glu	Glu	Met	Ile	Ala	Thr	Leu	Gln	His	Phe
				230					235					240
Met	Asp	Asp	Ile	Asn	Tyr	Ile	Asn	Val	Gly	Glu	Ile	Ala	Ser	Phe
				245					250					255
Ile	Ser	Ser	Thr	Asp	Tyr	Leu	Ser	Thr	Leu	Leu	Leu	Asp	Arg	Ile
				260					265					270
Ala	Ser	Val	Ala	Val	Gln	Gln	Ile	Glu	Lys	Ile	His	Pro	Phe	Thr
				275					280					285
Ile	Pro	Ala	Ile	Ile	Arg	Pro	Phe	Ser	Val	Leu	Asn	Tyr	Asp	Pro
				290					295					300
Pro	Gln	Arg	Asp	Glu	Phe	Leu	Gly	Thr	Cys	Val	Gln	His	Leu	Asn
				305					310					315
Ser	Tyr	Leu	Gly	Ile	Leu	Asp	Pro	Phe	Ile	Leu	Val	Phe	Leu	Gly
				320					325					330
Phe	Ser	Leu	Ala	Thr	Leu	Glu	Tyr	Phe	Pro	Glu	Asp	Leu	Leu	Lys
				335					340					345
Ala	Ile	Phe	Asn	Ile	Lys	Phe	Leu	Ala	Arg	Leu	Asp	Ser	Gln	Leu
				350					355					360
Glu	Ile	Leu	Ser	Pro	Ser	Arg	Ser	Ala	Arg	Val	Gln	Phe	His	Leu
				365					370					375
Met	Glu	Leu	Asn	Arg	Ser	Val	Cys	Leu	Glu	Cys	Pro	Glu	Phe	Gln
				380					385					390
Ile	Pro	Trp	Phe	His	Asp	Arg	Phe	Cys	Gln	Gln	Tyr	Asn	Lys	Gly
				395					400					405

```

Ile Gly Gly Met Asp Gly Thr Gln Gln Gln Ile Phe Lys Met Leu
410 415 420
Ala Glu Val Leu Gly Gly Ile Asn Cys Val Lys Ala Ser Val Leu
425 430 435
Thr Pro Tyr Tyr His Lys Val Asp Phe Glu Cys Ile Leu Asp Lys
440 445 450
Arg Lys Lys Pro Leu Pro Tyr Gly Ser His Asn Ile Ala Leu Gly
455 460 465
Gln Leu Pro Glu Met Pro Trp Glu Ser Asn Ile Glu Ile Val Gly
470 475 480
Ser Arg Leu Pro Pro Gly Ala Glu Arg Ile Ala Leu Glu Phe Leu
485 490 495
Asp Ser Lys Ala Leu Cys Arg Asn Ile Pro His Met Lys Gly Lys
500 505 510
Ser Ala Met Lys Lys Arg His Leu Glu Ile Leu Gly Tyr Arg Val
515 520 525
Ile Gln Ile Ser Gln Phe Glu Trp Asn Ser Met Ala Leu Ser Thr
530 535 540
Lys Asp Ala Arg Met Asp Tyr Leu Arg Glu Cys Ile Phe Gly Glu
545 550 555
Val Lys Ser Cys Leu
560

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<210> 37

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1932226

<400> 37

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Met Gly Val Pro Leu Gly Leu Gly Ala Ala Trp Leu Leu Ala Trp
1 5 10 15
Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg
20 25 30
Trp Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg
35 40 45
Leu Trp Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg
50 55 60
Ala Leu Gln Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala
65 70 75
Leu Tyr Pro Lys Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro
80 85 90
Val Pro Gly Pro Arg Arg Arg Asn Pro Arg Thr Thr Gln His Pro
95 100 105
Leu Ala Leu Leu Ala Arg Val Trp Val Leu Cys Lys Gly Trp Asn
110 115 120
Trp Arg Leu Ala Arg Ala Ser Gln Gly Leu Ala Ser His Leu Pro
125 130 135
Pro Trp Ala Ile His Thr Leu Ala Ser Trp Gly Leu Leu Arg Gly
140 145 150
Glu Arg Pro Thr Arg Ile Pro Arg Leu Leu Pro Arg Ser Gln Arg

```

	155	160	165
Gln Leu Gly Pro	Pro Ala Ser Arg Gln	Pro Leu Pro Gly Thr	Leu
	170	175	180
Ala Gly Arg Arg	Ser Arg Thr Arg Gln	Ser Arg Ala Leu Pro	Pro
	185	190	195
Trp Arg			

<210> 38

<211> 437

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1932647

<400> 38

Met Ser Ala Val	Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro	
1	5	10 15
Leu Pro Gly Val	Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln	
	20	25 30
His Val Trp Lys	Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys	
	35	40 45
Asn Thr Ser Cys	Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met	
	50	55 60
Leu Ile Glu Ser	Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly	
	65	70 75
Cys Thr Glu Ala	Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg	
	80	85 90
Met Gly Pro Gly	Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg	
	95	100 105
Gln Glu Asp Phe	Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp	
	110	115 120
Ala Pro Gln Pro	Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val	
	125	130 135
Cys Leu Ser Met	Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile	
	140	145 150
Cys Pro Lys Gly	Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu	
	155	160 165
Arg Gly Gly Gly	Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met	
	170	175 180
Pro Gln Pro Gly	Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly	
	185	190 195
Pro Val Gly Met	Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr	
	200	205 210
Cys His Arg Gly	Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln	
	215	220 225
Glu Pro Thr Asp	Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val	
	230	235 240
Gly Gln Val Cys	Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu	
	245	250 255
Thr Ser Thr Leu	Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala	
	260	265 270
Gln Asn Ser Gln	Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val	

275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn	
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu	Asn Ser Leu Pro Pro Gln	
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln	Cys Pro Thr Cys Val Gln	
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro	
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln	
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe	
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His	
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp	Trp Gly Val Val Cys Pro	
425	430	435
Ser Cys		

<210> 39

<211> 330

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2124245

<400> 39

Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Leu	
1 5 10 15	
Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro	
20 25 30	
Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile	
35 40 45	
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln	
50 55 60	
Val Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn	
65 70 75	
Asp Leu Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr	
80 85 90	
Leu Ile Val Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu	
95 100 105	
Tyr Phe Gly Ile Val Ser Val Arg Ile Leu Val His Glu Trp Pro	
110 115 120	
Met Thr Ser Gly Ser Ser Leu Gln Leu Ile Val Ile Gln Glu Glu	
125 130 135	
Val Val Glu Ile Asp Gly Lys Gln Val Gln Gln Lys Asp Val Thr	
140 145 150	
Glu Ile Asp Ile Leu Val Lys Asn Arg Gly Val Leu Arg His Ser	

Asn Tyr Thr Leu	155	Pro Leu Glu Glu Ser	160	Met Leu Tyr Ser Ile	165
Arg Asp Ser Asp	170	Ile Leu Phe Thr Leu	175	Pro Asn Leu Ser Lys	180
Glu Ser Val Ser	185	Ser Leu Gln Thr Thr	190	Ser Gln Tyr Leu Ile	195
Asn Val Glu Thr	200	Thr Val Asp Glu Asp	205	Val Leu Pro Gly Lys	210
Pro Glu Thr Pro	215	Leu Arg Ala Glu Pro	220	Pro Ser Ser Tyr Lys	225
Met Cys Gln Trp	230	Met Glu Lys Phe Arg	235	Lys Asp Leu Cys Arg	240
Trp Ser Asn Val	245	Phe Pro Val Phe Phe	250	Gln Phe Leu Asn Ile	255
Val Val Gly Ile	260	Thr Gly Ala Ala Val	265	Val Ile Thr Ile Leu	270
Val Phe Phe Pro	275	Val Ser Glu Tyr Lys	280	Gly Ile Leu Gln Leu	285
Lys Val Asp Val	290	Ile Pro Val Thr Ala	295	Ile Asn Leu Tyr Pro	300
Gly Pro Glu Lys	305	Arg Ala Glu Asn Leu	310	Glu Asp Lys Thr Cys	315
	320		325		330

<210> 40

<211> 148

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2132626

<400> 40

Met Glu Thr Gly	Ala	Leu	Arg	Arg	Pro	Gln	Leu	Leu	Pro	Leu	Leu
1	5					10					15
Leu Leu Leu Cys	Gly	Gly	Cys	Pro	Arg	Ala	Gly	Gly	Cys	Asn	Glu
	20					25					30
Thr Gly Met Leu	Arg	Leu	Pro	Leu	Cys	Gly	Lys	Ala	Phe	Ala	
	35					40					45
Asp Met Met Gly	Lys	Val	Asp	Val	Trp	Lys	Trp	Cys	Asn	Leu	Ser
	50					55					60
Glu Phe Ile Val	Tyr	Tyr	Glu	Ser	Phe	Thr	Asn	Cys	Thr	Glu	Met
	65					70					75
Glu Ala Asn Val	Val	Gly	Cys	Tyr	Trp	Pro	Asn	Pro	Leu	Ala	Gln
	80					85					90
Gly Phe Ile Thr	Gly	Ile	His	Arg	Gln	Phe	Phe	Ser	Asn	Cys	Thr
	95					100					105
Val Asp Arg Val	His	Leu	Glu	Asp	Pro	Pro	Asp	Glu	Val	Leu	Ile
	110					115					120
Pro Leu Ile Val	Ile	Pro	Val	Val	Leu	Thr	Val	Ala	Met	Ala	Gly
	125					130					135
Leu Val Val Trp	Arg	Ser	Lys	Arg	Thr	Asp	Thr	Leu	Leu		
	140					145					

<210> 41
 <211> 188
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2280639

<400> 41
 Met Ala Pro Pro Pro Pro Ser Pro Gln Leu Leu Leu Leu Ala Ala
 1 5 10 15
 Leu Ala Arg Leu Leu Gly Pro Ser Glu Val Met Ala Gly Pro Ala
 20 25 30
 Glu Glu Ala Gly Ala His Cys Pro Glu Ser Leu Trp Pro Leu Pro
 35 40 45
 Pro Gln Val Ser Pro Arg Val Thr Tyr Thr Arg Val Ser Pro Gly
 50 55 60
 Gln Ala Glu Asp Val Thr Phe Leu Tyr His Pro Cys Ala His Pro
 65 70 75
 Trp Leu Lys Leu Gln Leu Ala Leu Leu Ala Tyr Ala Cys Met Ala
 80 85 90
 Asn Pro Ser Leu Thr Pro Asp Phe Ser Leu Thr Gln Asp Arg Pro
 95 100 105
 Leu Val Leu Thr Ala Trp Gly Leu Ala Leu Glu Met Ala Trp Val
 110 115 120
 Glu Pro Ala Trp Ala Ala His Trp Leu Met Arg Arg Arg Arg Arg
 125 130 135
 Lys Gln Arg Lys Lys Lys Ala Trp Ile Tyr Cys Glu Ser Leu Ser
 140 145 150
 Gly Pro Ala Pro Ser Glu Pro Thr Pro Gly Arg Gly Arg Leu Cys
 155 160 165
 Arg Arg Gly Cys Val Gln Ala Leu Ala Leu Ala Phe Ala Leu Arg
 170 175 180
 Thr Gly Gly Pro Leu Ala Gln Arg
 185

<210> 42
 <211> 222
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2292356

<400> 42
 Met Ala Ala Ala Ala Leu Thr Ser Leu Ser Thr Ser Pro Leu Leu
 1 5 10 15
 Leu Gly Ala Pro Val Ala Ala Phe Ser Pro Glu Pro Gly Leu Glu
 20 25 30

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Pro Trp Lys Glu Ala Leu Val Arg Pro Pro Gly Ser Tyr Ser Ser
      35      40      45
Ser Ser Asn Ser Gly Asp Trp Gly Trp Asp Leu Ala Ser Asp Gln
      50      55      60
Ser Ser Pro Ser Thr Pro Ser Pro Pro Leu Pro Pro Glu Ala Ala
      65      70      75
His Phe Leu Phe Gly Glu Pro Thr Leu Arg Lys Arg Lys Ser Pro
      80      85      90
Ala Gln Val Met Phe Gln Cys Leu Trp Lys Ser Cys Gly Lys Val
      95     100     105
Leu Ser Thr Ala Ser Ala Met Gln Arg His Ile Arg Leu Val His
     110     115     120
Leu Gly Cys Gly Gly Ala Trp Gly Ala Ala Gly Pro Ala Gly Trp
     125     130     135
Leu Gly Leu Leu Gly Pro Ala Arg Pro Pro Leu Gln Leu Pro Leu
     140     145     150
Ala Gly Cys Val Ser Arg Arg Arg Gln Ala Glu Pro Glu Gln Ser
     155     160     165
Asp Gly Glu Glu Asp Phe Tyr Tyr Thr Glu Leu Asp Val Gly Val
     170     175     180
Asp Thr Leu Thr Asp Gly Leu Ser Ser Leu Thr Pro Val Phe Pro
     185     190     195
Glu Gly Phe His Ala Ser Leu Pro Ser Pro Ala Leu Lys Leu Arg
     200     205     210
Arg Leu Gly Gly Thr Arg Gln Pro Arg Gln Tyr Pro
     215     220

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<210> 43

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2349310

<400> 43

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Met Gly Pro Ser Ser Cys Leu Leu Leu Ile Leu Ile Pro Leu Leu
  1      5      10      15
Gln Leu Ile Asn Leu Gly Ser Thr Gln Cys Ser Leu Asp Ser Val
     20      25      30
Met Asp Lys Lys Ile Lys Asp Val Leu Asn Ser Leu Glu Tyr Ser
     35      40      45
Pro Ser Pro Ile Ser Lys Lys Leu Ser Cys Ala Ser Val Lys Ser
     50      55      60
Gln Gly Arg Pro Ser Ser Cys Pro Ala Gly Met Ala Val Thr Gly
     65      70      75
Cys Ala Cys Gly Tyr Gly Cys Gly Ser Trp Asp Val Gln Leu Glu
     80      85      90
Thr Thr Cys His Cys Gln Cys Ser Val Val Asp Trp Thr Thr Ala
     95     100     105
Arg Cys Cys His Leu Thr
     110

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<210> 44
 <211> 341
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2373227

<400> 44
 Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn
 1 5 10 15
 Leu Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro
 20 25 30
 Thr Glu Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr
 35 40 45
 Arg Ser Tyr Arg Ser Thr Ala Arg Thr Gly Leu Pro Arg Lys Thr
 50 55 60
 Arg Ile Ile Leu Glu Asp Glu Asn Asp Ala Met Ala Asp Ala Asp
 65 70 75
 Arg Leu Ala Gly Pro Ala Ala Ala Glu Leu Leu Ala Ala Thr Val
 80 85 90
 Ser Thr Gly Phe Ser Arg Ser Ser Ala Ile Asn Glu Glu Asp Gly
 95 100 105
 Ser Ser Glu Glu Gly Val Val Ile Asn Ala Gly Lys Asp Ser Thr
 110 115 120
 Ser Arg Glu Leu Pro Ser Ala Thr Pro Asn Thr Ala Gly Ser Ser
 125 130 135
 Ser Thr Arg Phe Ile Ala Asn Ser Gln Glu Pro Glu Ile Arg Leu
 140 145 150
 Thr Ser Ser Leu Pro Arg Ser Pro Gly Arg Ser Thr Glu Asp Leu
 155 160 165
 Pro Gly Ser Gln Ala Thr Leu Ser Gln Trp Ser Thr Pro Gly Ser
 170 175 180
 Thr Pro Ser Arg Trp Pro Ser Pro Ser Pro Thr Ala Met Pro Ser
 185 190 195
 Pro Glu Asp Leu Arg Leu Val Leu Met Pro Trp Gly Pro Trp His
 200 205 210
 Cys His Cys Lys Ser Gly Thr Met Ser Arg Ser Arg Ser Gly Lys
 215 220 225
 Leu His Gly Leu Ser Gly Arg Leu Arg Val Gly Ala Leu Ser Gln
 230 235 240
 Leu Arg Thr Glu His Lys Pro Cys Thr Tyr Gln Gln Cys Pro Cys
 245 250 255
 Asn Arg Leu Arg Glu Glu Cys Pro Leu Asp Thr Ser Leu Cys Thr
 260 265 270
 Asp Thr Asn Cys Ala Ser Gln Ser Thr Thr Ser Thr Arg Thr Thr
 275 280 285
 Thr Thr Pro Phe Pro Thr Ile His Leu Arg Ser Ser Pro Ser Leu
 290 295 300
 Pro Pro Ala Ser Pro Cys Pro Ala Leu Ala Phe Trp Lys Arg Val
 305 310 315
 Arg Ile Gly Leu Glu Asp Ile Trp Asn Ser Leu Ser Ser Val Phe
 320 325 330
 Thr Glu Met Gln Pro Ile Asp Arg Asn Gln Arg

335

340

<210> 45
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2457682

<400> 45
Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala
1 5 10 15
Ala Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg
20 25 30
Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala
35 40 45
Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala
50 55 60
Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val
65 70 75
Thr Val Gly Leu Tyr Leu Gln Glu Gly His Lys Val Pro Gln Phe
80 85 90
His Gly Lys Trp Pro Phe Ser Arg Phe Leu Phe Phe Gln Glu Pro
95 100 105
Ala Ser Ala Val Ala Ser Phe Leu Asn Gly Leu Ala Ser Leu Val
110 115 120
Met Leu Cys Arg Tyr Arg Thr Phe Val Pro Ala Ser Ser Pro Met
125 130 135
Tyr His Thr Cys Val Ala Phe Ala Trp Leu Ser Gly Arg
140 145

<210> 46
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2480426

<400> 46
Met Arg Pro Leu Leu Val Leu Leu Leu Leu Gly Leu Ala Ala Gly
1 5 10 15
Ser Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly
20 25 30
Leu Pro Gly Pro Arg Gly Asp Pro Gly Pro Arg Gly Glu Ala Gly
35 40 45
Pro Ala Gly Pro Thr Gly Leu Ala Gly Glu Cys Ser Val Pro Pro
50 55 60

Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu Ile Arg Val Pro Pro
 65 70 75
 Leu Ser Asp Ala Pro Leu Pro Ser Thr Ala Cys Trp
 80 85

<210> 47

<211> 383

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2503743

<400> 47

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu
 1 5 10 15
 Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro
 20 25 30
 Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
 35 40 45
 Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
 50 55 60
 Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
 65 70 75
 Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
 80 85 90
 Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile
 95 100 105
 Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
 110 115 120
 Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu

	290		295		300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys	Asp Ala Gln Pro Gly	Ala		
	305		310		315
Ser Gly Ser Gly	Val Tyr Val Arg Met	Trp Lys Arg Gln Gln	Gln		
	320		325		330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile	Phe Ser Gly His Gln	Trp		
	335		340		345
Val Asp Met Asn	Gly Ser Pro Gln Asp	Phe Asn Val Ala Val	Arg		
	350		355		360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Tyr Trp Ile Lys	Gly		
	365		370		375
Asn Tyr Leu Asp	Cys Arg Glu Gly				
	380				

<210> 48

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2537684

<400> 48

Met Leu Leu Pro	Ala Leu Cys Ala Trp	Leu Leu Trp Val Pro	Trp
1	5	10	15
Cys Leu Leu Val	Ala Gly Ser Gly Arg	Ser Gly Gly Glu Leu	Cys
	20	25	30
Cys Ser Ser Tyr	Gly Val Ser Val Ile	Ser Val Trp Ser Lys	Cys
	35	40	45
Ser Val Cys Arg	Cys Leu Met Gly Ser	Val Pro Arg Ile Phe	Phe
	50	55	60
Ala Phe Tyr Pro	Ile Ala Trp Leu Pro	Leu Pro Gly Ser Gln	Gly
	65	70	75
Cys Trp Ser Arg	Ser Trp Glu Trp Pro	Leu Val Glu Pro Ala	Ser
	80	85	90
Cys Leu Val Cys	Leu Cys Phe Thr Phe	Gly Val Leu Ser Gly	Val
	95	100	105
Val Ala Val Lys			

<210> 49

<211> 185

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2593853

<400> 49

Met Lys Phe Thr Ile Val Phe Ala Gly Leu Leu Gly Val Phe Leu

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1           5           10           15
Ala Pro Ala Leu Ala Asn Tyr Asn Ile Asn Val Asn Asp Asp Asn
20           25           30
Asn Asn Ala Gly Ser Gly Gln Gln Ser Val Ser Val Asn Asn Glu
35           40           45
His Asn Val Ala Asn Val Asp Asn Asn Asn Gly Trp Asp Ser Trp
50           55           60
Asn Ser Ile Trp Asp Tyr Gly Asn Gly Phe Ala Ala Thr Arg Leu
65           70           75
Phe Gln Lys Lys Thr Cys Ile Val His Lys Met Asn Lys Glu Val
80           85           90
Met Pro Ser Ile Gln Ser Leu Asp Ala Leu Val Lys Glu Lys Lys
95           100          105
Leu Gln Gly Lys Gly Pro Gly Gly Pro Pro Lys Gly Leu Met
110          115          120
Tyr Ser Val Asn Pro Asn Lys Val Asp Asp Leu Ser Lys Phe Gly
125          130          135
Lys Asn Ile Ala Asn Met Cys Arg Gly Ile Pro Thr Tyr Met Ala
140          145          150
Glu Glu Met Gln Glu Ala Ser Leu Phe Phe Tyr Ser Gly Thr Cys
155          160          165
Tyr Thr Thr Ser Val Leu Trp Ile Val Asp Ile Ser Phe Cys Gly
170          175          180
Asp Thr Val Glu Asn
185

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<210> 50

<211> 110

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2622354

<400> 50

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Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
1           5           10           15
Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20           25           30
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35           40           45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50           55           60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65           70           75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80           85           90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95           100          105
Cys Arg Ser Val Ser
110

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<210> 51
 <211> 126
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2641377

<400> 51
 Met Trp Leu Gly Ser Trp Leu Thr Ser Leu Leu Leu Ser Pro Tyr
 1 5 10 15
 Gly Ser Gly Trp Glu Lys Val Pro Cys Cys Val Thr Gly His Leu
 20 25 30
 Arg Ser Cys Ser Cys Cys Leu Leu Gly Leu Ala Gly Val Gln Ser
 35 40 45
 Asp His Phe Ser Glu Gly Phe Phe Ser Glu Tyr Ser Ser Asp Val
 50 55 60
 Leu Pro Trp Gly Arg Arg Ser Phe Leu Pro Gln Gly Asp Ala Ser
 65 70 75
 Leu Leu Ala Cys Glu Cys Phe Leu His Leu Gln Val Val Trp Gly
 80 85 90
 Gln Phe Cys Leu Leu Glu Ala Trp Ala Gly Phe Thr Glu Gly Ser
 95 100 105
 Met Pro Ala Pro Ser Cys Arg Val His Phe Trp Cys Arg Val Asn
 110 115 120
 Thr Cys Ala Phe Met Ser
 125

<210> 52
 <211> 488
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2674857

<400> 52
 Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly
 1 5 10 15
 Leu Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys Pro Tyr
 20 25 30
 Thr Lys Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp Leu
 35 40 45
 Leu Tyr His Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe
 50 55 60
 Pro Gly Val Val Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala
 65 70 75
 Val Phe Ser Ser Pro Ala Val Tyr Val Leu Ser Leu Leu Glu Met
 80 85 90
 Ser Lys Phe Tyr Ser Gln Leu Ile Val Arg Gly Val Leu Gly Leu
 95 100 105

Gly Val Ile Phe	Gly Leu Trp Thr Leu Gln Lys Glu Val Arg Arg	110	115	120
His Phe Gly Ala	Met Val Ala Thr Met Phe Cys Trp Val Thr Ala	125	130	135
Met Gln Phe His	Leu Met Phe Tyr Cys Thr Arg Thr Leu Pro Asn	140	145	150
Val Leu Ala Leu	Pro Val Val Leu Leu Ala Leu Ala Ala Trp Leu	155	160	165
Arg His Glu Trp	Ala Arg Phe Ile Trp Leu Ser Ala Phe Ala Ile	170	175	180
Ile Val Phe Arg	Val Glu Leu Cys Leu Phe Leu Gly Leu Leu Leu	185	190	195
Leu Leu Ala Leu	Gly Asn Arg Lys Val Ser Val Val Arg Ala Leu	200	205	210
Arg His Ala Val	Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr Val	215	220	225
Ala Val Asp Ser	Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly	230	235	240
Lys Val Leu Trp	Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp	245	250	255
Gly Thr Ser Pro	Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg	260	265	270
Gly Leu Gly Cys	Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp	275	280	285
Arg Arg Thr His	Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	290	295	300
Leu Tyr Ser Leu	Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr	305	310	315
Ala Phe Pro Met	Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr	320	325	330
Leu Leu Asn Asn	Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser	335	340	345
Leu Leu Val Ile	Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala	350	355	360
Thr Ala Leu Tyr	Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala	365	370	375
Met Gln Arg Leu	His Gln Leu Val Pro Pro Gln Thr Asp Val Leu	380	385	390
Leu His Ile Asp	Val Ala Ala Ala Gln Thr Gly Val Ser Arg Phe	395	400	405
Leu Gln Val Asn	Ser Ala Trp Arg Tyr Asp Lys Arg Glu Asp Val	410	415	420
Gln Pro Gly Thr	Gly Met Leu Ala Tyr Thr His Ile Leu Met Glu	425	430	435
Ala Ala Pro Gly	Leu Leu Ala Leu Tyr Arg Asp Thr His Arg Val	440	445	450
Leu Ala Ser Val	Val Gly Thr Thr Gly Val Ser Leu Asn Leu Thr	455	460	465
Gln Leu Pro Pro	Phe Asn Val His Leu Gln Thr Lys Leu Val Leu	470	475	480
Leu Glu Arg Leu	Pro Arg Pro Ser	485		

<210> 53

<211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2758485

<400> 53
 Met Ser Pro Arg Arg Thr Leu Pro Arg Pro Leu Ser Leu Cys Leu
 1 5 10 15
 Ser Leu Cys Leu Cys Leu Cys Leu Ala Ala Ala Leu Gly Ser Ala
 20 25 30
 Gln Ser Gly Ser Cys Arg Asp Lys Lys Asn Cys Lys Val Val Phe
 35 40 45
 Ser Gln Gln Glu Leu Arg Lys Arg Leu Thr Pro Leu Gln Tyr His
 50 55 60
 Val Thr Gln Glu Lys Gly Thr Glu Ser Ala Phe Glu Gly Glu Tyr
 65 70 75
 Thr His His Lys Asp Pro Gly Ile Tyr Lys Cys Val Val Cys Gly
 80 85 90
 Thr Pro Leu Phe Lys Ser Glu Thr Lys Phe Asp Ser Gly Ser Gly
 95 100 105
 Trp Pro Ser Phe His Asp Val Ile Asn Ser Glu Ala Ile Thr Phe
 110 115 120
 Thr Asp Asp Phe Ser Tyr Gly Met His Arg Val Glu Thr Ser Cys
 125 130 135
 Ser Gln Cys Gly Ala His Leu Gly His Ile Phe Asp Asp Gly Pro
 140 145 150
 Arg Pro Thr Gly Lys Arg Tyr Cys Ile Asn Ser Ala Ala Leu Ser
 155 160 165
 Phe Thr Pro Ala Asp Ser Ser Gly Thr Ala Glu Gly Gly Ser Gly
 170 175 180
 Val Ala Ser Pro Ala Gln Ala Asp Lys Ala Asp Ser Glu Ser Asn
 185 190 195
 Gly Glu

<210> 54
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2763296

<400> 54
 Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser
 1 5 10 15
 Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu
 20 25 30
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Tyr Trp Ser Met Arg Leu Gln Ala Arg Gly Gly Pro

```

          50          55          60
Ser Pro Leu Lys Ser Asn Ser Asp Ser Ala Arg Leu Pro Ile Ser
          65          70          75
Ser Gly Ser Thr Ser Ser Ser Arg Ile
          80

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<210> 55

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2779436

<400> 55

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Met Gln Leu Gly Thr Gly Leu Leu Leu Ala Ala Val Leu Ser Leu
 1          5          10          15
Gln Leu Ala Ala Ala Glu Ala Ile Trp Cys His Gln Cys Thr Gly
          20          25          30
Phe Gly Gly Cys Ser His Gly Ser Arg Cys Leu Arg Asp Ser Thr
          35          40          45
His Cys Val Thr Thr Ala Thr Arg Val Leu Ser Asn Thr Glu Asp
          50          55          60
Leu Pro Leu Val Thr Lys Met Cys His Ile Gly Cys Pro Asp Ile
          65          70          75
Pro Ser Leu Gly Leu Gly Pro Tyr Val Ser Ile Ala Cys Cys Gln
          80          85          90
Thr Ser Leu Cys Asn His Asp
          95

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<210> 56

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2808528

<400> 56

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Met Ala Ala Ser Leu Gly Gln Val Leu Ala Leu Val Leu Val Ala
 1          5          10          15
Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ala
          20          25          30
Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu
          35          40          45
Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro
          50          55          60
Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu
          65          70          75

```

Ala	Ser	Thr	Asp	Leu	Thr	Leu	Ala	Val	Pro	Ile	Cys	Asn	Ser	Leu
				80					85					90
Ala	Ile	Ile	Phe	Thr	Leu	Ile	Val	Gly	Lys	Ala	Leu	Gly	Glu	Asp
				95					100					105
Ile	Gly	Gly	Lys	Arg	Ala	Val	Ala	Gly	Met	Val	Leu	Thr	Val	Ile
				110					115					120
Gly	Ile	Ser	Leu	Cys	Ile	Thr	Ser	Ser	Val	Ser	Lys	Thr	Gln	Gly
				125					130					135
Gln	Gln	Ser	Thr	Leu										
				140										

<210> 57
 <211> 285
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2809230

<400> 57

Met	Glu	Val	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Phe	Leu	Cys	Arg	Ala
1				5					10					15
Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30
Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val
				35					40					45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu
				50					55					60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala
				65					70					75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val
				80					85					90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile
				95					100					105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val
				110					115					120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly
				125					130					135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn
				140					145					150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu
				155					160					165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg
				170					175					180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly
				185					190					195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln
				200					205					210
Lys	Tyr	Ser	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg
				215					220					225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu
				230					235					240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Gln

	245		250		255
Glu Asp Glu Pro	Glu Asn Asp Ala Lys	Lys Ile Glu Ala Leu	Leu		
	260		265		270
Asn Leu Pro Arg	Asn Pro Ser Val Ile	Asp Lys Gln Asp Lys	Asp		
	275		280		285

<210> 58
 <211> 262
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2816821

<400> 58

Met Thr Gln Pro Val	Pro Arg Leu Ser Val	Pro Ala Ala Leu Ala
1	5	10
Leu Gly Ser Ala Ala	Leu Gly Ala Ala Phe	Ala Thr Gly Leu Phe
	20	25
Leu Gly Arg Arg Cys	Pro Pro Trp Arg Gly	Arg Arg Glu Gln Cys
	35	40
Leu Leu Pro Pro Glu	Asp Ser Arg Leu Trp	Gln Tyr Leu Leu Ser
	50	55
Arg Ser Met Arg Glu	His Pro Ala Leu Arg	Ser Leu Arg Leu Leu
	65	70
Thr Leu Glu Gln Pro	Gln Gly Asp Ser Met	Met Thr Cys Glu Gln
	80	85
Ala Gln Leu Leu Ala	Asn Leu Ala Arg Leu	Ile Gln Ala Lys Lys
	95	100
Ala Leu Asp Leu Gly	Thr Phe Thr Gly Tyr	Ser Ala Leu Ala Leu
	110	115
Ala Leu Ala Leu Pro	Ala Asp Gly Arg Val	Val Thr Cys Glu Val
	125	130
Asp Ala Gln Pro Pro	Glu Leu Gly Arg Pro	Leu Trp Arg Gln Ala
	140	145
Glu Ala Glu His Lys	Ile Asp Leu Arg Leu	Lys Pro Ala Leu Glu
	155	160
Thr Leu Asp Glu Leu	Leu Ala Ala Gly Glu	Ala Gly Thr Phe Asp
	170	175
Val Ala Val Val Asp	Ala Asp Lys Glu Asn	Cys Ser Ala Tyr Tyr
	185	190
Glu Arg Cys Leu Gln	Leu Leu Arg Pro Gly	Gly Ile Leu Ala Val
	200	205
Leu Arg Val Leu Trp	Arg Gly Lys Val Leu	Gln Pro Pro Lys Gly
	215	220
Asp Val Ala Ala Glu	Cys Val Arg Asn Leu	Asn Glu Arg Ile Arg
	230	235
Arg Asp Val Arg Val	Tyr Ile Ser Leu Leu	Pro Leu Gly Asp Gly
	245	250
Leu Thr Leu Ala Phe	Lys Ile	
	260	

<210> 59
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2817268

<400> 59
 Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu
 1 5 10 15
 Met Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp
 20 25 30
 Trp Arg Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile
 35 40 45
 Asp Thr Tyr Leu Asn Ala Ala Leu Asp Leu Leu Gly Gly Glu Asp
 50 55 60
 Gly Leu Cys Gln Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro
 65 70 75
 Arg Tyr Gly Tyr Lys Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro
 80 85 90
 Leu Phe Gly Val His Leu Asn Ile Gly Ile Pro Ser Leu Thr Lys
 95 100 105
 Cys Cys Asn Gln His Asp Arg Cys Tyr Glu Thr Cys Gly Lys Ser
 110 115 120
 Lys Asn Asp Cys Asp Glu Glu Phe Gln Tyr Cys Leu Ser Lys Ile
 125 130 135
 Cys Arg Asp Val Gln Lys Thr Leu Gly Leu Thr Gln His Val Gln
 140 145 150
 Ala Cys Glu Thr Thr Val Glu Leu Leu Phe Asp Ser Val Ile His
 155 160 165
 Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg Ala Ala Cys Arg
 170 175 180
 Cys His Tyr Glu Glu Lys Thr Asp Leu
 185

<210> 60
 <211> 257
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2923165

<400> 60
 Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
 1 5 10 15
 Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Thr Glu Pro Leu
 20 25 30
 Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
 35 40 45

```

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
    50                    55                    60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
    65                    70                    75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
    80                    85                    90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
    95                    100                   105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
   110                   115                   120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
   125                   130                   135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
   140                   145                   150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
   155                   160                   165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
   170                   175                   180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
   185                   190                   195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
   200                   205                   210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
   215                   220                   225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
   230                   235                   240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
   245                   250                   255
Ser Arg

```

<210> 61

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2949822

<400> 61

```

Met Pro Phe Ser Trp Met Val Ile Ile Leu Gly Phe Leu Cys Gly
  1          5          10          15
Leu Ser Gly Gln Leu Gln Ile Met Asn Thr Leu Ser Ser Leu Pro
  20          25          30
Ile Val Leu Leu Val Ser Ser Ser Cys Leu Ile Leu Ala Arg Met
  35          40          45
Ser Tyr Ser Ile Leu Thr Ser Ser Tyr Gly Gly Gly Val Phe Ile
  50          55          60
Leu Leu Asp Leu Lys Arg Asn Thr Ser Lys Val Ser Pro Leu Met
  65          70          75
Met Met Phe Ala Ile Gly His
  80

```


<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2992192

<400> 62
Met Ala Ala Pro Trp Arg Arg Trp Pro Thr Gly Leu Leu Ala Val
1 5 10 15
Leu Arg Pro Leu Leu Thr Cys Arg Pro Leu Gln Gly Thr Thr Leu
20 25 30
Gln Arg Asp Val Leu Leu Phe Glu His Asp Arg Gly Arg Phe Phe
35 40 45
Thr Ile Leu Gly Leu Phe Cys Ala Gly Gln Gly Val Phe Trp Ala
50 55 60
Ser Met Ala Val Ala Ala Val Ser Arg Pro Pro Val Pro Val Gln
65 70 75
Pro Leu Asp Ala Glu Val Pro Asn Arg Gly Pro Phe Asp Leu Arg
80 85 90
Ser Ala Leu Trp Arg Tyr Gly Leu Ala Val Gly Cys Gly Ala Ile
95 100 105
Gly Ala Leu Val Leu Gly Ala Gly Leu Leu Phe Ser Leu Arg Ser
110 115 120
Val Arg Ser Val Val Leu Arg Ala Gly Gly Gln Gln Val Thr Leu
125 130 135
Thr Thr His Ala Pro Phe Gly Leu Gly Ala His Phe Thr Val Pro
140 145 150
Leu Lys Gln Val Ser Cys Met Ala His Arg Gly Glu Val Pro Ala
155 160 165
Met Leu Pro Leu Lys Val Lys Gly Arg Arg Phe Tyr Phe Leu Leu
170 175 180
Asp Lys Thr Gly His Phe Pro Asn Thr Lys Leu Phe Asp Asn Thr
185 190 195
Val Gly Ala Tyr Arg Ser Leu
200

<210> 63
<211> 450
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2992458

<400> 63
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15
Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr				

<210> 64
 <211> 322
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 3044710

<400> 64

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp
1				5					10					15
Thr	Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu
			20						25					30
Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser
			35						40					45
Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala
			50						55					60
Cys	Arg	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu
			65						70					75
Thr	Ala	Leu	Lys	Ala	Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val
			80						85					90
Gly	Asp	Gly	Phe	Val	Val	Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys
			95						100					105
Cys	Gly	Lys	Asn	Gly	Val	Gly	Val	Leu	Ile	Trp	Lys	Val	Pro	Val
			110						115					120
Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	Tyr	Asn	Ser	Ser	Asp	Thr	Trp
			125						130					135
Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile	Thr	Thr	Lys	Asp	Pro	Ile
			140						145					150
Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	Glu	Phe	Ile	Val	Ser
			155						160					165
Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser	Thr	Ile	Pro	Ala
			170						175					180
Pro	Thr	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	Ile	Pro	Arg
			185						190					195
Arg	Lys	Lys	Leu	Ile	Cys	Val	Thr	Glu	Val	Phe	Met	Glu	Thr	Ser
			200						205					210
Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	Glu	Asn	Lys	Ala	Ala
			215						220					225
Phe	Lys	Asn	Glu	Ala	Ala	Gly	Phe	Gly	Gly	Val	Pro	Thr	Ala	Leu
			230						235					240
Leu	Val	Leu	Ala	Leu	Leu	Phe	Phe	Gly	Ala	Ala	Ala	Gly	Leu	Gly
			245						250					255
Phe	Cys	Tyr	Val	Lys	Arg	Tyr	Val	Lys	Ala	Phe	Pro	Phe	Thr	Asn
			260						265					270
Lys	Asn	Gln	Gln	Lys	Glu	Met	Ile	Glu	Thr	Lys	Val	Val	Lys	Glu
			275						280					285
Glu	Lys	Ala	Asn	Asp	Ser	Asn	Pro	Asn	Glu	Glu	Ser	Lys	Lys	Thr
			290						295					300
Asp	Lys	Asn	Pro	Glu	Glu	Ser	Lys	Ser	Pro	Ser	Lys	Thr	Thr	Val
			305						310					315
Arg	Cys	Leu	Glu	Ala	Glu	Val								
			320											

<210> 65
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 3120415

<400> 65
 Met Lys Leu Ala Ala Leu Leu Gly Leu Cys Val Ala Leu Ser Cys
 1 5 10 15
 Ser Ser Ala Ala Ala Phe Leu Val Gly Ser Ala Lys Pro Val Ala
 20 25 30
 Gln Pro Val Ala Ala Leu Glu Ser Ala Ala Glu Ala Gly Ala Gly
 35 40 45
 Thr Leu Ala Asn Pro Leu Gly Thr Leu Asn Pro Leu Lys Leu Leu
 50 55 60
 Leu Ser Ser Leu Gly Ile Pro Val Asn His Leu Ile Glu Gly Ser
 65 70 75
 Gln Lys Cys Val Ala Glu Leu Gly Pro Gln Ala Val Gly Ala Val
 80 85 90
 Lys Ala Leu Lys Ala Leu Leu Gly Ala Leu Thr Val Phe Gly
 95 100

<210> 66
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 126758

<400> 66
 Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys
 1 5 10 15
 Ser Tyr Ser Ala Thr Ala Phe Leu Ile Asn Lys Val Pro Leu Pro
 20 25 30
 Val Asp Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe
 35 40 45
 Met Asp Pro Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val
 50 55 60
 Glu His Leu Val Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly
 65 70 75
 Pro Glu Ala Ser Glu Ala Val Lys Lys Leu Leu Glu Ala Leu Ser
 80 85 90
 His Leu Val

<210> 67
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 674760

<400> 67
 Met Thr Ala Gly Gln Phe Pro Ala Leu Val Ser Leu Ala Leu Leu
 1 5 10 15
 Leu Asp Gly Gly Arg Arg Ala Ser Ala Arg Arg Asn Arg Gly His
 20 25 30
 Leu Trp Val Phe Cys Thr Ser Phe Leu Leu Ala Pro Trp Glu Val
 35 40 45
 Glu Asp Val Gly Trp Lys Lys Gly Leu Asp Leu Pro Pro Ser Ser
 50 55 60
 Ser Pro Pro Ser Pro Lys Glu Leu Ala Leu Gln
 65 70

<210> 68
 <211> 394
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1229438

<400> 68
 Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr
 1 5 10 15
 Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu
 20 25 30
 Ser Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln
 35 40 45
 Gln Glu Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu
 50 55 60
 Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly
 65 70 75
 Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val
 80 85 90
 Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr Asp Gly
 95 100 105
 Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro Leu
 110 115 120
 Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Leu
 125 130 135
 Val Arg Tyr Leu Leu His Arg Ala Lys Lys Gly Leu Gly Met Arg
 140 145 150
 Arg Ala Asp Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Phe
 155 160 165
 Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser His

	170		175		180
Tyr Glu His Trp	Thr Phe Phe Gln Ala	Tyr Tyr Tyr Cys Phe	Ile		
	185		190		195
Thr Leu Thr Thr	Ile Gly Phe Gly Asp	Tyr Val Ala Leu Gln	Lys		
	200		205		210
Asp Gln Ala Leu	Gln Thr Gln Pro Gln	Tyr Val Ala Phe Ser	Phe		
	215		220		225
Val Tyr Ile Leu	Thr Gly Leu Thr Val	Ile Gly Ala Phe Leu	Asn		
	230		235		240
Leu Val Val Leu	Arg Phe Met Thr Met	Asn Ala Glu Asp Glu	Lys		
	245		250		255
Arg Asp Ala Glu	His Arg Ala Leu Leu	Thr Arg Asn Gly Gln	Ala		
	260		265		270
Gly Gly Gly Gly	Gly Gly Gly Ser Ala	His Thr Thr Asp Thr	Ala		
	275		280		285
Ser Ser Thr Ala	Ala Ala Gly Gly Gly	Gly Phe Arg Asn Val	Tyr		
	290		295		300
Ala Glu Val Leu	His Phe Gln Ser Met	Cys Ser Cys Leu Trp	Tyr		
	305		310		315
Lys Ser Arg Glu	Lys Leu Gln Tyr Ser	Ile Pro Met Ile Ile	Pro		
	320		325		330
Arg Asp Leu Ser	Thr Ser Asp Thr Cys	Val Glu Gln Ser His	Ser		
	335		340		345
Ser Pro Gly Gly	Gly Gly Arg Tyr Ser	Asp Thr Pro Ser Arg	Arg		
	350		355		360
Cys Leu Cys Ser	Gly Ala Pro Arg Ser	Ala Ile Ser Ser Val	Ser		
	365		370		375
Thr Gly Leu His	Ser Leu Ser Thr Phe	Arg Gly Leu Met Lys	Arg		
	380		385		390
Arg Ser Ser Val					

<210> 69

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1236935

<400> 69

Met Cys Pro Phe Phe	Pro Leu Thr Ser	Leu Ile Val Phe	Leu Ile
1	5	10	15
Leu Phe Phe Lys Thr	Ile Ala Ser Ser	Gly Ser Gly Gly	Ser Cys
	20	25	30
Leu Gly Leu Pro Lys	Cys Trp Asp Tyr	Arg Arg Glu His	Arg Ala
	35	40	45
Arg Pro Thr Ile Val	Phe Ser Lys His	Val Tyr Thr Tyr	Ser Met
	50	55	60
Arg Met Gln Ile Glu	Ile Ser Thr Asn	Ile Ser Gln	
	65	70	

<210> 70
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1359283

<400> 70
 Met Arg Leu Thr Gly Leu Thr Leu Leu Leu Ser Leu Met Glu Ser
 1 5 10 15
 Leu Gly Gln Val Glu Asp Arg Phe Phe Ser Thr His Arg Arg Phe
 20 25 30
 Pro His His Thr Pro Ile Ser Gly Leu Leu Cys Arg Glu Phe Ser
 35 40 45
 Leu Pro Lys Arg Ser Gly Val Pro Trp Thr Arg Val Leu Ile Ser
 50 55 60
 Cys Ile Trp Arg Ser Gly Ala Gly Lys Arg Met
 65 70

<210> 71
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1450703

<400> 71
 Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
 20 25 30
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala

	170		175		180
Gly Lys Glu Leu	Gln Asn Ala His Asn	Gly Val Asn Gln Ala	Ser		
	185		190		195
Lys Glu Ala Asn	Gln Leu Leu Asn Gly	Asn His Gln Ser Gly	Ser		
	200		205		210
Ser Ser His Gln	Gly Gly Ala Thr Thr	Thr Pro Leu Ala Ser	Gly		
	215		220		225
Ala Ser Val Asn	Thr Pro Phe Ile Asn	Leu Pro Ala Leu Trp	Arg		
	230		235		240
Ser Val Ala Asn	Ile Met Pro				
	245				

<210> 72
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1910668

<400> 72	
Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe Leu Ser Tyr Leu	
1 5 10 15	
Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly Ser Thr Leu	
20 25 30	
Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg Pro Trp	
35 40 45	
Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Glu Asn	
50 55 60	
Gln Tyr Glu Lys Trp Gly Gln Gly Thr His Ser Ser Leu	
65 70	

<210> 73
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1955143

<400> 73	
Met Gly Arg Leu Arg Tyr Phe Phe Ser Leu Leu Leu Arg Trp	
1 5 10 15	
Gly Gln Leu Leu Gly Ala Asp Glu Phe Cys Cys His Lys Ser Tyr	
20 25 30	
Ile Ala His Leu Val Cys Thr Glu Ser Ala Ile Leu Asn Pro Gly	
35 40 45	
His Ala Leu Glu Leu Tyr Lys Lys Asn Leu Gln Val Ser Ile Leu	
50 55 60	

Ser Pro Tyr Pro Thr Asp Pro Ile His Leu
65 70

<210> 74
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1961637

<400> 74
Met Met Phe Thr Ser Leu Ser Leu Ala Leu Pro Phe Leu Leu Gln
1 5 10 15
Thr Met Leu Cys Leu Arg Ala Leu Leu Ile Ala Val Pro His Gly
20 25 30
His Asp Trp Asn Arg Asp Ala Thr Ser Phe Tyr Thr Ser Thr Val
35 40 45
Ser Trp Val Lys Ser Phe Phe Leu Phe Val Leu Asp Gly Val Ser
50 55 60
Leu Leu Leu Pro Arg Leu Glu
65

<210> 75
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1990762

<400> 75
Met Trp Pro Thr Thr Trp Ala Trp Ser Trp Val Gln Thr Leu Thr
1 5 10 15
Leu Ala Leu Leu Ile Ser Cys Val Thr Leu Gly Gln Leu Ile Thr
20 25 30
Thr Leu Gln Val Ser Phe Leu Ile Cys Glu Met Asp Val Ile Ile
35 40 45
Gly Cys Asp Glu Met Ile Pro Ser Glu Ser Leu Val Leu Leu Trp
50 55 60
Pro Pro Pro Leu Leu Leu Leu Gly Glu Phe Trp Ile Trp Asn Pro
65 70 75
Val Ser Arg Ile Leu Phe Trp Leu Cys His Val Pro Ala Gly Gln
80 85 90
Leu

<210> 76
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1994131

<400> 76
 Met Asn Glu Trp Trp Leu Leu Leu Leu Leu His Leu His Pro Pro
 1 5 10 15
 Arg Val Ile Ser Pro Phe Trp Phe Ile Val Ser Val Leu Thr Ala
 20 25 30
 Cys Asp Asn Arg Lys Tyr Ile Leu Leu Arg Thr Val Pro Val Phe
 35 40 45
 Ser Phe Pro Glu Asn Thr Tyr Phe Asp Val Gly
 50 55

<210> 77
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1997745

<400> 77
 Met Pro Leu Phe Leu Ser Ile Pro Ser Leu Phe Leu Thr Leu Ser
 1 5 10 15
 Gly Leu Gly Leu Ala Val Gln Ser Pro Ala Gly Gly Cys Trp Gly
 20 25 30
 Leu Ser Leu Cys Arg His Cys Val Phe Leu Arg Gly Cys Pro Gln
 35 40 45
 Asn Thr Pro Pro Ala Pro Trp Gly Ser Ser Gly Ser His Phe Ser
 50 55 60
 Trp Ser Leu Arg Ser Gln Lys Gln Leu Leu Gln Glu Ala Lys Lys
 65 70 75
 Arg Leu Gly Trp Leu Leu Val Leu Met Met Ala Phe Ile Leu Leu
 80 85 90
 Gly His Phe Gly Tyr Ile His Gly His Cys Phe His Leu Ser Phe
 95 100 105
 Leu Pro Val Pro Pro Leu Pro
 110

<210> 78
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2009035

<400> 78

```

Met Met Leu Gln Pro Val Asp Leu Leu Gln Ser Tyr Leu Leu Leu
 1          5          10          15
Leu Tyr Cys Trp Ser Phe Ser Leu Leu Phe Thr Leu Leu Cys Asn
          20          25          30
Ala Val Arg Asn Asp Phe Phe His Lys Leu Phe Ser Ile Tyr Trp
          35          40          45
Met Tyr Asn Leu Thr His Ser Lys His
          50

```

<210> 79

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2009152

<400> 79

```

Met Lys Phe Tyr Ala Val Leu Leu Ser Ile Cys Leu Leu Leu Ser
 1          5          10          15
Cys Trp Cys Ala Cys His Val Arg Asp Cys Asn Leu Ile Cys Leu
          20          25          30
Phe Ser Thr Val Lys Ala Ile Thr Arg Glu Leu Leu Gln Leu Pro
          35          40          45
Ser Tyr Val Lys Arg Phe Phe Phe Asn Ser Leu Arg
          50          55

```

<210> 80

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2061752

<400> 80

```

Met Gln Arg Leu Gly Lys Ala Pro Gly Thr Trp Gln Ala Ile Ser
 1          5          10          15
Lys Cys Trp Leu Leu Leu Leu Leu Ser Leu Pro Phe Ser Gln Ser
          20          25          30
Ile Ile Ile Ser Leu Arg Ala Gly Thr Met Ser Tyr Leu Pro Leu
          35          40          45
Tyr Phe Pro Gln Tyr Phe Pro
          50

```

<210> 81
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2061933

<400> 81
 Met Lys Leu Leu Leu Leu Lys Leu Asp Phe Phe Ile Leu Leu Gly
 1 5 10 15
 Ser Glu Glu Ser Arg Cys Leu Val Asp Val Gln Tyr Val Ile Phe
 20 25 30
 Phe Leu Ile Glu Cys Val His Leu Lys Ser Ser Leu Thr Phe Leu
 35 40 45
 Glu Arg Leu Leu Ser Ile Asn Asn Gly Ile Leu Glu Glu Lys Trp
 50 55 60
 Phe Phe Lys Ser

<210> 82
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2081422

<400> 82
 Met Lys Pro Leu Ile Pro Phe Leu Ser Pro Pro Pro Leu Leu Pro
 1 5 10 15
 Leu Thr Phe Phe Leu Ser Ser Leu Leu Leu Ser Pro Leu Cys Arg
 20 25 30
 Ala Leu Gly Thr Ser Gln Ala Val Pro Pro Leu Arg Ala Leu Ser
 35 40 45
 Val Thr Asp Ala His Gly Ser Leu Leu Leu His Pro Lys Thr Leu
 50 55 60
 Ala Cys Pro Cys Leu
 65

<210> 83
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

<223> Incyte Clone No: 2101278

<400> 83

Met	Arg	Ala	Asp	Arg	Leu	Leu	Pro	Ile	Ser	Ala	Leu	Cys	Leu	Leu
1				5					10				15	
Tyr	Thr	Pro	Gly	Gly	Ala	Leu	Glu	Pro	Ala	Gln	Val	Gly	Tyr	Thr
			20						25				30	
Ile	Phe	Leu	Asn	Ser	Ile	Trp	Leu	Pro	Ala	Tyr	Phe	Phe	His	Leu
			35						40				45	
Phe	Thr	Val	Ile	Ser	Gly	Val	Phe	Leu	Phe	Ile				
			50						55					

<210> 84

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2121353

<400> 84

Met	Pro	Ala	Leu	Pro	Pro	Gly	Phe	Ser	Gln	Ala	Gly	Ser	Cys	Val
1				5					10				15	
Pro	Thr	Gly	Ser	Ser	Leu	Val	Leu	Cys	Leu	Leu	Ala	Ala	Ser	Leu
			20						25				30	
Leu	Leu	Phe	Val	Pro	Thr	Leu	Ala	Leu	Leu	Thr	Gly	Ala	Thr	Thr
			35						40				45	
Cys	Trp	Cys	Leu	His	Asn	Lys	Arg	Leu	Ala	Leu	Arg	Pro	Leu	Ala
			50						55				60	
Trp	Gln	Gly	Leu	Trp	Gly	Leu	Val	Ser	Thr	Arg	Leu	Ser	His	Gly
			65						70				75	
Arg	Thr	Ser	Phe	Tyr	Phe	Asn	Ser	Leu	Pro	Leu	Gln	Thr	Asn	Ser
			80						85				90	
Ser	Thr	Cys	Gln	Asn	His	Ser	Trp	Asp	Ser	Gly	Ala	Arg	Ala	Thr
			95						100				105	
Ala	Leu	Ala	Ser	Gly	Arg	Thr	Gln	Glu	Gly	Gly	Val	Gly	Ser	Val
			110						115				120	

<210> 85

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2241736

<400> 85

Met	Asn	Ser	Leu	Val	Leu	Phe	Leu	Gly	His	Leu	Gly	Leu	Leu	Ile
1				5					10				15	

```

Lys Asp Cys Val Leu Leu Phe Ala Met Ser Lys Val Ser Gln Lys
      20                      25                      30
Gln Lys Val Leu Gly Pro Phe Gly Ser Pro Glu Leu Glu Ser Leu
      35                      40                      45
Gly Ile Gly Pro Arg Tyr Leu His Phe His Arg Phe Leu Val Gly
      50                      55                      60
Asp Phe Leu Gln Ala Lys Val
      65

```

```

<210> 86
<211> 62
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte Clone No: 2271935

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```

<400> 86
Met Ala Trp Leu Ser Phe Ala Ala Val Glu Met Thr Leu Leu Leu
  1          5          10          15
His Ser Ser Ser Leu Leu Ser Phe Ala Lys Val Val Leu Ser Leu
      20          25          30
Pro Glu Ile Arg Pro Phe Gly Asp Gly Asn Phe Ser Leu Lys Gln
      35          40          45
Ser Ser Lys Gln Asn Pro Asn Pro Ala Arg Val Gly Arg Lys Ser
      50          55          60
Met Phe

```

```

<210> 87
<211> 75
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<223> Incyte Clone No: 2295344

```

```

<400> 87
Met Met Ile Leu Leu Ser Leu Leu Val Ala Leu Ile Ser Val Ser
  1          5          10          15
Leu Val Phe Leu Gly Leu Val Arg Phe Ser Arg Glu Asp Phe Ser
      20          25          30
Phe Pro Leu Trp Arg Glu Lys Ala Phe Tyr Gln His Ser Ser Ser
      35          40          45
Ser Val Gly Glu Arg Leu Gln Ala Leu Arg Lys His Ala Phe Thr
      50          55          60
Leu Phe Gly Thr Ile Pro Leu Leu Val Thr Val Pro Gln Val Pro
      65          70          75

```

<210> 88
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2303994

<400> 88
Met Asn Ser Ile Phe Phe Leu Ser Leu Cys Leu Pro Leu Trp Val
1 5 10 15
Ser Leu Leu Trp Ala Lys Pro Leu Glu Met His Lys Thr Ser Arg
20 25 30
His Gly Phe Trp Gln Lys Leu His Asp Phe Lys Leu Ala Leu Leu
35 40 45
Leu Leu Thr Phe His Arg Glu Lys Ile Phe Pro Leu Lys Lys Thr
50 55 60
Gly Leu Val Ile Phe Ser Leu Val Ala Leu Ser Arg Asp Ile Ser
65 70 75
Ala Leu His Tyr Thr
80

<210> 89
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2497805

<400> 89
Met Arg Pro Ala Arg Leu Gly Pro Arg Cys Ser Asp Leu Asp Phe
1 5 10 15
Gly Leu Val Leu Ser Ser Trp Leu Arg Leu Ala Arg Cys Pro Leu
20 25 30
Glu Ser Ser Phe Gly Phe Ala Phe Phe Val Cys Leu Phe Ser Pro
35 40 45
Asn Phe Cys Gln Thr
50

<210> 90
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2646362

<400> 90

```

Met Trp Trp Ala Leu Cys Ser Met Leu Pro Leu Leu Gly Cys Ala
 1          5          10          15
Cys Ser Ser Gly Cys Trp Gly Ser Gly Pro Thr Pro Leu Leu Ala
          20          25          30
Glu Pro Thr Phe Leu Cys Val Ser Ser Arg Pro His Asn Pro Leu
          35          40          45
Ser Phe Leu Ser Val Leu Pro Cys Ser Arg Gly Pro Gly Pro Ser
          50          55          60
Gly Leu Gln Gly Asp Gly Ala Gly Leu Pro Ala His Leu Gly Pro
          65          70          75
Leu Ser Cys Ile Cys Leu Pro Ser Leu Leu Cys Asp Leu Gly Glu
          80          85          90
Arg Gln Cys Pro Leu Trp Ala Val Arg Ser Thr Gln Cys Leu Ile
          95          100          105
Ala Gly Lys Lys Val Leu Gln Arg Leu Cys Pro
          110          115

```

<210> 91

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2657146

<400> 91

```

Met Ile Cys Gln Cys Leu Arg Leu Leu Leu Val Leu Val Thr Leu
 1          5          10          15
Leu Ile Cys Phe Ser Pro Asp Arg Leu Thr Cys Pro Leu Asn Ser
          20          25          30
Ala Val Val Leu Ala Ser Tyr Ala Val Gln Cys Lys Ser Gln Arg
          35          40          45
Glu His Phe Thr Asp Gly Gln Val Val Leu Ile Ser Val Trp Arg
          50          55          60
Lys Ser Leu Val Pro Pro Ala
          65

```

<210> 92

<211> 538

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2755786

<400> 92

```

Met Ala Gly Ala Arg-Ala Ala Ala Ala Ala Ala Ser Ala Gly Ser
 1          5          10          15

```


Ser	Ala	Ser	Ser	Gly	Asn	Gln	Pro	Pro	Gln	Glu	Leu	Gly	Leu	Gly
				20					25					30
Glu	Leu	Leu	Glu	Glu	Phe	Ser	Arg	Thr	Gln	Tyr	Arg	Ala	Lys	Asp
				35					40					45
Gly	Ser	Gly	Thr	Gly	Gly	Ser	Lys	Val	Glu	Arg	Ile	Glu	Lys	Arg
				50					55					60
Cys	Leu	Glu	Leu	Phe	Gly	Arg	Asp	Tyr	Cys	Phe	Ser	Val	Ile	Pro
				65					70					75
Asn	Thr	Asn	Gly	Asp	Ile	Cys	Gly	His	Tyr	Pro	Arg	His	Ile	Val
				80					85					90
Phe	Leu	Glu	Tyr	Glu	Ser	Ser	Glu	Lys	Glu	Lys	Asp	Thr	Phe	Glu
				95					100					105
Ser	Thr	Val	Gln	Val	Ser	Lys	Leu	Gln	Asp	Leu	Ile	His	Arg	Ser
				110					115					120
Lys	Met	Ala	Arg	Cys	Arg	Gly	Arg	Phe	Val	Cys	Pro	Val	Ile	Leu
				125					130					135
Phe	Lys	Gly	Lys	His	Ile	Cys	Arg	Ser	Ala	Thr	Leu	Ala	Gly	Trp
				140					145					150
Gly	Glu	Leu	Tyr	Gly	Arg	Ser	Gly	Tyr	Asn	Tyr	Phe	Phe	Ser	Gly
				155					160					165
Gly	Ala	Asp	Asp	Ala	Trp	Ala	Asp	Val	Glu	Asp	Val	Thr	Glu	Glu
				170					175					180
Asp	Cys	Ala	Leu	Arg	Ser	Gly	Asp	Thr	His	Leu	Phe	Asp	Lys	Val
				185					190					195
Arg	Gly	Tyr	Asp	Ile	Lys	Leu	Leu	Arg	Tyr	Leu	Ser	Val	Lys	Tyr
				200					205					210
Ile	Cys	Asp	Leu	Met	Val	Glu	Asn	Lys	Lys	Val	Lys	Phe	Gly	Met
				215					220					225
Asn	Val	Thr	Ser	Ser	Glu	Lys	Val	Asp	Lys	Ala	Gln	Arg	Tyr	Ala
				230					235					240
Asp	Phe	Thr	Leu	Leu	Ser	Ile	Pro	Tyr	Pro	Gly	Cys	Glu	Phe	Phe
				245					250					255
Lys	Glu	Tyr	Lys	Asp	Arg	Asp	Tyr	Met	Ala	Glu	Gly	Leu	Ile	Phe
				260					265					270
Asn	Trp	Lys	Gln	Asp	Tyr	Val	Asp	Ala	Pro	Leu	Ser	Ile	Pro	Asp
				275					280					285
Phe	Leu	Thr	His	Ser	Leu	Asn	Ile	Asp	Trp	Ser	Gln	Tyr	Gln	Cys
				290					295					300
Trp	Asp	Leu	Val	Gln	Gln	Thr	Gln	Asn	Tyr	Leu	Lys	Leu	Leu	Leu
				305					310					315
Ser	Leu	Val	Asn	Ser	Asp	Asp	Asp	Ser	Gly	Leu	Leu	Val	His	Cys
				320					325					330
Ile	Ser	Gly	Trp	Asp	Arg	Thr	Pro	Leu	Phe	Ile	Ser	Leu	Leu	Arg
				335					340					345
Leu	Ser	Leu	Trp	Ala	Asp	Gly	Leu	Ile	His	Thr	Ser	Leu	Lys	Pro
				350					355					360
Thr	Glu	Ile	Leu	Tyr	Leu	Thr	Val	Ala	Tyr	Asp	Trp	Phe	Leu	Phe
				365					370					375
Gly	His	Met	Leu	Val	Asp	Arg	Leu	Ser	Lys	Gly	Glu	Glu	Ile	Phe
				380					385					390
Phe	Phe	Cys	Phe	Asn	Phe	Leu	Lys	His	Ile	Thr	Ser	Glu	Glu	Phe
				395					400					405
Ser	Ala	Leu	Lys	Thr	Gln	Arg	Arg	Lys	Ser	Leu	Pro	Ala	Arg	Asp
				410					415					420
Gly	Gly	Phe	Thr	Leu	Glu	Asp	Ile	Cys	Met	Leu	Arg	Arg	Lys	Asp
				425					430					435
Arg	Gly	Ser	Thr	Thr	Ser	Leu	Gly	Ser	Asp	Phe	Ser	Leu	Val	Met

	440		445		450
Glu Ser Ser Pro	Gly Ala Thr Gly Ser	Phe Thr Tyr Glu Ala Val			
	455		460		465
Glu Leu Val Pro	Ala Gly Ala Pro Thr	Gln Ala Ala Trp Leu Ala			
	470		475		480
Ala Leu Ser Asp	Arg Glu Thr Arg Leu	Gln Glu Val Arg Ser Ala			
	485		490		495
Phe Leu Ala Ala	Tyr Ser Ser Thr Val	Gly Leu Arg Ala Val Ala			
	500		505		510
Pro Ser Pro Ser	Gly Ala Ile Gly Gly	Leu Leu Glu Gln Phe Ala			
	515		520		525
Arg Gly Val Gly	Leu Arg Ser Ile Ser	Ser Asn Ala Leu			
	530		535		

<210> 93
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2831245

<400> 93	
Met Glu Met Lys Gly Ser Arg Val Trp Leu Leu Leu Phe Met	
1 5 10 15	
Trp Lys Ala Arg Pro Thr Phe Phe Gln Ser Cys Val Val Pro Phe	
20 25 30	
Ile Leu Ser Pro Gln Asn Cys Val Gln Thr His Ser Leu Gly Pro	
35 40 45	
Gly Val Trp Leu Gly Val Phe Pro Ser Gly Ser Leu His	
50 55	

<210> 94
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 3116250

<400> 94	
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met	
1 5 10 15	
Leu Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg	
20 25 30	
Gly His Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu	
35 40 45	
Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro	
50 55 60	

Arg	Arg	Lys	Phe	Met	Thr	Val	Ser	Gly	Leu	Pro	Lys	Lys	Gln	Cys
				65					70					75
Pro	Cys	Asp	His	Phe	Lys	Gly	Asn	Val	Lys	Lys	Thr	Arg	His	Gln
				80					85					90
Arg	His	His	Arg	Lys	Pro	Asn	Lys	His	Ser	Arg	Ala	Cys	Gln	Gln
				95					100					105
Phe	Leu	Lys	Gln	Cys	Gln	Leu	Arg	Ser	Phe	Ala	Leu	Pro	Leu	
				110					115					

<210> 95

<211> 128

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3129630

<400> 95

Met	Ala	Tyr	Ser	Thr	Val	Gln	Arg	Val	Ala	Leu	Ala	Ser	Gly	Leu
1				5					10					15
Val	Leu	Ala	Leu	Ser	Leu	Leu	Leu	Pro	Lys	Ala	Phe	Leu	Ser	Arg
				20					25					30
Gly	Lys	Arg	Gln	Glu	Pro	Pro	Pro	Thr	Pro	Glu	Gly	Lys	Leu	Gly
				35					40					45
Arg	Phe	Pro	Pro	Met	Met	His	His	His	Gln	Ala	Pro	Ser	Asp	Gly
				50					55					60
Gln	Thr	Pro	Gly	Ala	Arg	Phe	Gln	Arg	Ser	His	Leu	Ala	Glu	Ala
				65					70					75
Phe	Ala	Lys	Ala	Lys	Gly	Ser	Gly	Gly	Gly	Ala	Gly	Gly	Gly	Gly
				80					85					90
Ser	Gly	Arg	Gly	Leu	Met	Gly	Gln	Ile	Ile	Pro	Ile	Tyr	Gly	Phe
				95					100					105
Gly	Ile	Phe	Leu	Tyr	Ile	Leu	Tyr	Ile	Leu	Phe	Lys	Val	Ser	Arg
				110					115					120
Ile	Ile	Leu	Ile	Ile	Leu	His	Gln							
				125										

<210> 96

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 007632

<400> 96

Met	Tyr	Lys	Leu	Ala	Ser	Cys	Cys	Leu	Leu	Phe	Ile	Gly	Phe	Leu
1				5					10					15
Asn	Pro	Leu	Leu	Ser	Leu	Pro	Leu	Leu	Asp	Ser	Arg	Glu	Ile	Ser

	20		25		30
Phe	Gln	Leu	Ser	Ala	Pro
	35		40		45
Glu	Leu	Glu	Arg	Ala	Ser
	50		55		60
Gly	Ala	Glu	Arg	Gly	Asp
	65		70		75
Asn	Ile	Phe	Asn	Pro	Arg
	80		85		90
Ser	Gly	Gln	Asp	Pro	Asn
	95		100		105
Ile	Trp	Lys	Pro	Tyr	Lys
	110		115		120
Lys	Tyr	Cys	Val		

<210> 97
 <211> 182
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1236968

<400> 97

Met	Trp	Pro	Leu	Ser	Ser	Asp	Ser	Ser	Trp	Ser	Leu	Trp	Ile	Ser
1			5						10					15
Thr	Gly	Met	Ala	Pro	Ala	Pro	Ser	Ser	Ser	Thr	Arg	Ser	Phe	Ser
			20						25					30
Glu	Ser	Leu	Lys	Gln	Lys	Leu	Val	Arg	Val	Leu	Glu	Glu	Asn	Leu
			35						40					45
Ile	Leu	Ser	Glu	Lys	Ile	Gln	Gln	Leu	Glu	Glu	Gly	Ala	Ala	Ile
			50						55					60
Ser	Ile	Val	Ser	Gly	Gln	Gln	Ser	His	Thr	Tyr	Asp	Asp	Leu	Leu
			65						70					75
His	Lys	Asn	Gln	Gln	Leu	Thr	Met	Gln	Val	Ala	Cys	Leu	Asn	Gln
			80						85					90
Glu	Leu	Ala	Gln	Leu	Lys	Lys	Leu	Glu	Lys	Thr	Val	Ala	Ile	Leu
			95						100					105
His	Glu	Ser	Gln	Arg	Ser	Leu	Val	Val	Thr	Asn	Glu	Tyr	Leu	Leu
			110						115					120
Gln	Gln	Leu	Asn	Lys	Glu	Pro	Lys	Gly	Tyr	Ser	Gly	Lys	Ala	Leu
			125						130					135
Leu	Pro	Pro	Glu	Lys	Gly	His	His	Leu	Gly	Arg	Ser	Ser	Pro	Phe
			140						145					150
Gly	Lys	Ser	Thr	Leu	Ser	Ser	Ser	Ser	Pro	Val	Ala	His	Glu	Thr
			155						160					165
Gly	Gln	Tyr	Leu	Ile	Gln	Ser	Val	Leu	Asp	Ala	Ala	Pro	Glu	Pro
			170						175					180
Gly	Leu													

<210> 98
 <211> 237
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1334153

<400> 98
 Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala
 1 5 10 15
 Ala Val Glu Ser Leu Ser Cys Val Pro Cys Asn Ser Trp Glu Lys
 20 25 30
 Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
 35 40 45
 Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
 50 55 60
 Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
 65 70 75
 Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
 80 85 90
 Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
 95 100 105
 Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
 110 115 120
 Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
 125 130 135
 Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
 140 145 150
 Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
 155 160 165
 Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
 170 175 180
 Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
 185 190 195
 Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
 200 205 210
 Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
 215 220 225
 Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
 230 235

<210> 99
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1396975

<400> 99
 Met Arg Pro Gly Pro Met Leu Gln Ala Arg Val Ser Ile Pro Ala

1	5	10	15
Ala Leu Gly Thr	Leu Phe Pro Arg Pro Gly Trp Ala Pro Gly Glu		
	20	25	30
Val Ser Ser Glu Ile	Ser Ser Arg Asp Leu Leu Asn Pro His Pro		
	35	40	45
Ser Thr Pro Ser Cys	Cys Ser Gln Ser Trp Ser Pro Met Ser Val		
	50	55	60
Leu Glu Pro Asp Ser	Arg Gly Pro Pro Ile Ser Leu Thr His		
	65	70	75
Thr Gly Ile His Thr	Pro Gln Lys Thr Ser Gln Met Arg Pro Asp		
	80	85	90
Ser Gly Ser Arg Gly	Met Cys Phe Cys Pro Cys Lys Gly Phe Gly		
	95	100	105
Glu Gly Gly Asn Ile	Val Glu Ala Gly Lys Ser Pro Gln Thr Cys		
	110	115	120
Ala His Ala Pro Pro	Ala Leu Arg Phe His Ser Ala Phe Ser Glu		
	125	130	135
Cys Pro Cys Cys Thr	Gln Thr Thr Gly Gln Glu Arg Pro Ser Leu		
	140	145	150
Pro Leu Gln Pro Leu	Ser Leu Pro Phe Asn		
	155	160	

<210> 100

<211> 148

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1501749

<400> 100

Met Ala Ala Ser Pro	Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1	5 10 15
Leu Ala Leu Leu Leu	Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
	20 25 30
Gly Asn Lys Leu Lys	Leu Met Leu Gln Lys Arg Glu Ala Pro Val
	35 40 45
Pro Thr Lys Thr Lys	Val Ala Val Asp Glu Asn Lys Ala Lys Glu
	50 55 60
Phe Leu Gly Ser Leu	Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
	65 70 75
Thr Arg Pro Glu Val	Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
	80 85 90
Gly Phe Asp Glu Ala	Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
	95 100 105
Asn Arg Asp Arg Asn	Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
	110 115 120
Arg His Tyr Asp Glu	Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
	125 130 135
Gly Phe Arg His Gly	Ala Ser Val Asn Tyr Asp Asp Tyr
	140 145

<210> 101
 <211> 170
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1575240

<400> 101
 Met Thr Pro Thr Lys Arg Glu Pro Pro Ala Ala Pro Leu Leu Leu
 1 5 10 15
 Arg Val Leu Pro Gln Leu Ser Ala Met Ser Leu Arg Leu Ser Thr
 20 25 30
 Arg Arg Glu Asp Met Ile Gly Gln Thr Ser Gly Met Cys Ser Phe
 35 40 45
 Cys Ser Phe Gln Asn Met Arg Gly Glu Ser Ile Trp Leu Leu Cys
 50 55 60
 Leu Glu Glu Glu Gly Ala Gly Leu Cys Gln Asn Ser Leu Asp Lys
 65 70 75
 Arg Phe Ser Gln Lys Glu Gly Cys Ser Asp Asp Lys Ser Pro Leu
 80 85 90
 His His Phe Pro Trp Leu Ser Asp Ala Pro Pro Ser Ser His Ala
 95 100 105
 Arg Thr Ser Glu Ile Arg Leu Pro Pro Asp Ile Thr Gln Pro Cys
 110 115 120
 Leu Thr Lys Arg Gln Trp Phe Ile Pro Ser Leu Gly Glu Lys Arg
 125 130 135
 Gly Asn Ala Lys Leu Leu His Gln Leu Leu Ile Leu Leu Pro Ala
 140 145 150
 Arg Asn Pro Gly Tyr Leu Gln Val Ser Leu Pro Leu Val Trp Ser
 155 160 165
 Trp Leu Ser Leu Phe
 170

<210> 102
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1647884

<400> 102
 Met Gly Ala Ala Ala Trp Ala Arg Pro Leu Ser Val Ser Phe Leu
 1 5 10 15
 Leu Leu Leu Leu Pro Leu Pro Gly Met Pro Ala Gly Ser Trp Asp
 20 25 30
 Pro Ala Gly Tyr Leu Leu Tyr Cys Pro Cys Met Gly Lys Ala Ser
 35 40 45
 Gln Ala Leu Cys Ser Asp Gly Glu Thr Glu Ala Gly Arg Gly Lys
 50 55 60

Ala	Thr	Pro	Gln	Met	Arg	Pro	Glu	Thr	Pro	Ser	Gln	Val	Gln	Glu
				65					70					75
Arg	Thr	Ser	Glu	Arg	Asp	Gly	Ala	Cys	Ser	Ser	Pro	Leu	Cys	Leu
				80					85					90
Ser	Cys	Lys	Gly	Thr	Glu	Gly	Pro	Thr	Cys	Pro	Thr	Phe	His	Leu
				95					100					105
Thr	Asp	Glu	Lys	Thr	Glu	Ala	Gly	Arg	Gly	Tyr	Val	Thr	Cys	Leu
				110					115					120
Arg	Ser	Lys	Pro	Val	Gln	Gly	Pro	Val	Asn	Gly	Val	Ser	Gly	Ala
				125					130					135
Gly	Leu	Asp	Val	Thr	Asp	Pro	Arg	Trp	Leu	Leu	Val	Ile	Phe	His
				140					145					150

<210> 103

<211> 142

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1661144

<400> 103

Met	Gly	Cys	Leu	Val	Trp	Gly	Pro	Ser	Trp	Pro	Pro	Leu	Ser	Leu
1				5					10					15
Leu	Ala	Ser	Leu	Leu	His	Ser	Gly	Ile	Ala	Gly	Arg	Cys	Leu	Leu
				20					25					30
Cys	Leu	Phe	Lys	Gly	Leu	Ala	Ala	Ala	Ala	Ser	Leu	Gln	Ile	Arg
				35					40					45
Asp	Leu	Ala	Ser	Arg	Leu	Thr	Thr	Gly	Pro	Arg	Thr	Cys	Arg	Val
				50					55					60
Gln	Pro	Pro	Pro	His	Pro	Gln	Ser	Ser	Pro	Pro	Trp	Pro	Gly	Pro
				65					70					75
Pro	Gly	Ala	Glu	Thr	Cys	Arg	Pro	Leu	Ser	Arg	Thr	Val	Gly	Gly
				80					85					90
Val	Cys	Pro	Ser	Asp	Trp	Pro	Val	Ser	Trp	Leu	Leu	Leu	Pro	Pro
				95					100					105
Leu	Pro	Glu	Val	Val	Thr	Cys	Ser	Cys	Pro	Arg	Ile	Lys	Ala	Arg
				110					115					120
Pro	Glu	Arg	Thr	Pro	Glu	Leu	Leu	Cys	Ala	Trp	Gly	Gly	Arg	Gly
				125					130					135
Lys	His	Ser	Gln	Leu	Val	Ala								
				140										

<210> 104

<211> 110

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1685409

<400> 104

Met	Glu	Thr	Gly	Arg	Leu	Leu	Ser	Leu	Ser	Ser	Leu	Pro	Leu	Val
1				5					10					15
Leu	Leu	Gly	Trp	Glu	Tyr	Ser	Ser	Gln	Thr	Leu	Asn	Leu	Val	Pro
				20					25					30
Ser	Thr	Ser	Ile	Leu	Ser	Phe	Val	Pro	Phe	Ile	Pro	Leu	His	Leu
				35					40					45
Val	Leu	Phe	Ala	Leu	Trp	Tyr	Leu	Pro	Val	Pro	His	His	Leu	Tyr
				50					55					60
Pro	Gln	Gly	Leu	Gly	Asp	His	Ala	Ala	Glu	Ala	Glu	Lys	Gly	Lys
				65					70					75
Arg	Glu	Glu	Gly	Gly	Thr	Gln	Val	Ala	Leu	Trp	Leu	Arg	Val	Gln
				80					85					90
Pro	Ser	Cys	Pro	Ser	Pro	Val	Cys	Leu	Glu	Pro	Val	Pro	Pro	Arg
				95					100					105
Ser	Arg	Phe	Leu	Leu										
				110										

<210> 105

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1731419

<400> 105

Met	Ser	Arg	Ala	Gly	Met	Leu	Gly	Val	Val	Cys	Ala	Leu	Leu	Val
1				5					10					15
Trp	Ala	Tyr	Leu	Ala	Val	Gly	Lys	Leu	Val	Val	Arg	Met	Thr	Phe
				20					25					30
Thr	Glu	Leu	Cys	Thr	His	His	Pro	Trp	Ser	Leu	Arg	Cys	Glu	Ser
				35					40					45
Phe	Cys	Arg	Ser	Arg	Val	Thr	Ala	Cys	Leu	Pro	Ala	Pro	Ala	Pro
				50					55					60
Trp	Leu	Arg	Pro	Phe	Leu	Cys	Pro	Met	Leu	Phe	Ser	Asp	Arg	Asn
				65					70					75
Pro	Val	Glu	Cys	His	Leu	Phe	Gly	Glu	Ala	Val	Ser	Asp	Pro	Val
				80					85					90
Cys	Lys	Gly	Leu	Leu	Pro	His	Tyr	Phe	Trp	His	Pro	Thr	Phe	Phe
				95					100					105
Pro	Val	Lys	Ala	Asn	Cys	Leu	Val	Ser	Phe	Cys	Pro	Thr	Thr	Val
				110					115					120

<210> 106

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2650265

<400> 106

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Met Ala Arg Phe Trp Val Cys Val Ala Gly Ala Gly Phe Phe Leu
  1          5          10          15
Ala Phe Leu Val Leu His Ser Arg Phe Cys Gly Ser Pro Val Leu
          20          25          30
Arg Asn Phe Thr Phe Ala Val Ser Trp Arg Thr Glu Lys Ile Leu
          35          40          45
Tyr Arg Leu Asp Val Gly Trp Pro Lys His Pro Glu Tyr Phe Thr
          50          55          60
Gly Thr Thr Phe Cys Val Ala Val Asp Ser Leu Asn Gly Leu Val
          65          70          75
Tyr Ile Gly Gln Arg Gly Asp Asn Ile Pro Lys Ile Leu Val Phe
          80          85          90
Thr Glu Asp Gly Tyr Phe Leu Arg Ala Trp Asn Tyr Thr Val Asp
          95          100          105
Thr Pro His Gly Ile Phe Ala Ala Ser Thr Leu Tyr Glu Gln Ser
          110          115          120
Val Trp Ile Thr Asp Val Gly Ser Gly Met Tyr Ser Asn Ile Tyr
          125          130          135

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<210> 107

<211> 301

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2677129

<400> 107

```

Met Leu Met Ile Ile Ile Ile Glu Pro Phe Ser Val Leu Ile Leu
  1          5          10          15
Phe Lys Ser Gly Ile Leu Ala Asp Phe Phe Ala Leu Leu Leu Leu
          20          25          30
Ile Asn Phe Phe Leu Val Ser Phe Phe Leu Ala Tyr Pro Leu Phe
          35          40          45
Asn Asn Gln Ile Asn Ser Arg Ser Met Asn Glu Ile Lys Asn Leu
          50          55          60
Gln Tyr Leu Pro Arg Thr Ser Glu Pro Arg Glu Val Leu Phe Glu
          65          70          75
Asp Arg Thr Arg Ala His Ala Asp His Val Gly Gln Gly Phe Asp
          80          85          90
Trp Gln Ser Thr Ala Ala Val Gly Val Leu Lys Ala Val Gln Phe
          95          100          105
Gly Glu Trp Ser Asp Gln Pro Arg Ile Thr Lys Asp Val Ile Cys
          110          115          120
Phe His Ala Glu Asp Phe Thr Asp Val Val Gln Arg Leu Gln Leu
          125          130          135
Asp Leu His Glu Pro Pro Val Ser Gln Cys Val Gln Trp Val Asp
          140          145          150

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Glu	Ala	Lys	Leu	Asn	Gln	Met	Arg	Arg	Glu	Gly	Ile	Arg	Tyr	Ala	
				155					160					165	
Arg	Ile	Gln	Leu	Cys	Asp	Asn	Asp	Ile	Tyr	Phe	Ile	Pro	Arg	Asn	
				170					175					180	
Val	Ile	His	Gln	Phe	Lys	Thr	Val	Ser	Ala	Val	Cys	Ser	Leu	Ala	
				185					190					195	
Trp	His	Ile	Arg	Leu	Lys	Gln	Tyr	His	Pro	Val	Val	Glu	Ala	Thr	
				200					205					210	
Gln	Asn	Thr	Glu	Ser	Asn	Ser	Asn	Met	Asp	Cys	Gly	Leu	Thr	Gly	
				215					220					225	
Lys	Arg	Glu	Leu	Glu	Val	Asp	Ser	Gln	Cys	Val	Arg	Ile	Lys	Thr	
				230					235					240	
Glu	Ser	Glu	Glu	Ala	Cys	Thr	Glu	Ile	Gln	Leu	Leu	Thr	Thr	Ala	
				245					250					255	
Ser	Ser	Ser	Phe	Pro	Pro	Ala	Ser	Glu	Leu	Asn	Leu	Gln	Gln	Asp	
				260					265					270	
Gln	Lys	Thr	Gln	Pro	Ile	Pro	Val	Leu	Lys	Val	Glu	Ser	Arg	Leu	
				275					280					285	
Asp	Ser	Asp	Gln	Gln	His	Asn	Leu	Gln	Glu	His	Ser	Thr	Thr	Ser	
				290					295					300	
Val															

<210> 108

<211> 103

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3151073

<400> 108

Met	Ser	Phe	Val	Pro	Gly	Leu	Leu	Leu	Cys	Phe	Val	Leu	Leu	Leu	
1				5					10					15	
Cys	Val	Ser	Pro	Val	Tyr	Leu	Pro	Ser	Arg	Ser	Pro	Ser	Thr	Phe	
				20					25					30	
Pro	Ile	Ser	Glu	Pro	Leu	Ser	Phe	Ile	Gly	Met	Ser	Ala	Trp	Pro	
				35					40					45	
Gln	Cys	Ser	Pro	Ile	Tyr	Ser	Gln	Thr	Pro	Gly	Leu	Ala	Tyr	Glu	
				50					55					60	
Pro	Ser	Ser	Phe	Pro	Lys	Arg	Arg	Tyr	Trp	Val	Cys	Thr	Leu	His	
				65					70					75	
Glu	Ile	Lys	Trp	Glu	Cys	Pro	Arg	Ser	Arg	Arg	Thr	Ser	Asp	Ala	
				80					85					90	
Val	His	Ala	Asn	Lys	Leu	Gly	Leu	Pro	Leu	Lys	Ile	Ile			
				95					100						

<210> 109

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3170095

<400> 109

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Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr
 1           5           10           15
Gln Val Ile Pro Ala Ser Ala Gly Gly Ser Lys Cys Val Ser Asn
          20           25           30
Thr Pro Gly Tyr Cys Arg Thr Cys Cys His Trp Gly Glu Thr Ala
          35           40           45
Leu Phe Met Cys Asn Ala Ser Arg Lys Cys Cys Ile Ser Tyr Ser
          50           55           60
Phe Leu Pro Lys Pro Asp Leu Pro Gln Leu Ile Gly Asn His Trp
          65           70           75
Gln Ser Arg Arg Arg Asn Thr Gln Arg Lys Asp Lys Lys Gln Gln
          80           85           90
Thr Thr Val Thr Ser
          95

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<210> 110

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3475168

<400> 110

```

Met Ser Pro Ser Pro Arg Trp Gly Phe Leu Cys Val Leu Phe Thr
 1           5           10           15
Ala Val His Pro Ala Pro Ser Thr Ala Pro Val Gln Asp Lys Cys
          20           25           30
Pro Val Asn Thr Trp Glu Ala Met Gln Ala Ser Ser Gln Gln Leu
          35           40           45
Leu Gln Thr Asp Pro Arg Pro Lys Pro Phe Leu Leu Pro Pro Leu
          50           55           60
Pro Pro Leu Leu Leu Ile Ser Ala Gly Thr Glu Val Ser Ser Leu
          65           70           75
Val Phe Gln Lys Ser Pro Leu His Thr Gln Pro Glu Gly Ala Ile
          80           85           90
Lys Thr Ala Gly Gln Pro Thr Ser Val His Ser Lys Val Leu Ser
          95          100          105
Lys Gly Ser Leu Leu Leu Gly Glu
          110

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<210> 111

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3836893

<400> 111

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Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val
  1          5          10          15
Ser Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu
          20          25          30
Leu Lys Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu
          35          40          45
Glu Lys Phe Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp
          50          55          60
Gly Glu Met Pro Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys
          65          70          75
Asn Ser His Pro Val Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr
          80          85          90
His Asp His Gly Leu Leu Arg Val Arg Met Val Asn Leu Gln Val
          95          100          105
Glu Asp Ser Gly Leu Tyr Gln Cys Val Ile Tyr Gln Pro Pro Lys
          110          115          120
Glu Pro His Met Leu Phe Asp Arg Ile Arg Leu Val Val Thr Lys
          125          130          135
Gly Phe Ser Gly Thr Pro Gly Ser Asn Glu Asn Ser Thr Gln Asn
          140          145          150
Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys Ala Leu Cys Pro Leu
          155          160          165
Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro Pro Lys Ser Thr
          170          175          180
Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu Thr Asn Val
          185          190          195
Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile Leu Leu
          200          205          210
Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu Phe
          215          220          225
Ala Val Thr Leu Arg Ser Phe Val Pro
          230

```

<210> 112

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 4072159

<400> 112

```

Met Val Leu Pro Leu Pro Trp Leu Ser Arg Tyr His Phe Leu Arg
  1          5          10          15
Leu Leu Leu Pro Ser Trp Ser Leu Ala Pro Gln Gly Ser His Gly
          20          25          30
Cys Cys Ser Gln Asn Pro Lys Ala Ser Met Glu Glu Gln Thr Asn
          35          40          45

```

```

Ser Arg Gly Asn Gly Lys Met Thr Ser Pro Pro Arg Gly Pro Gly
      50                      55                      60
Thr His Arg Thr Ala Glu Leu Ala Arg Ala Glu Glu Leu Leu Glu
      65                      70                      75
Gln Gln Leu Glu Leu Tyr Gln Ala Leu Leu Glu Gly Gln Glu Gly
      80                      85                      90
Ala Trp Glu Ala Gln Ala Leu Val Leu Lys Ile Gln Lys Leu Lys
      95                      100                     105
Glu Gln Met Arg Arg His Gln Glu Ser Leu Gly Gly Gly Ala
      110                     115

```

<210> 113
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1003916

```

<400> 113
Met Ala Ser Ser Leu Thr Cys Thr Gly Val Ile Trp Ala Leu Leu
  1      5      10      15
Ser Phe Leu Cys Ala Ala Thr Ser Cys Val Gly Phe Phe Met Pro
      20      25      30
Tyr Trp Leu Trp Gly Ser Gln Leu Gly Lys Pro Val Ser Phe Gly
      35      40      45
Thr Phe Arg Arg Cys Ser Tyr Pro Val His Asp Glu Ser Arg Gln
      50      55      60
Met Met Val Met Val Glu Glu Cys Gly Arg Tyr Ala Ser Phe Gln
      65      70      75
Gly Ile Pro Ser Ala Glu Trp Arg Ile Cys Thr Ile Val Thr Gly
      80      85      90
Leu Gly Cys Gly Leu Leu Leu Leu Val Ala Leu Thr Ala Leu Met
      95     100     105
Gly Cys Cys Val Ser Asp Leu Ile Ser Arg Thr Val Gly Arg Val
     110     115     120
Ala Gly Gly Ile Gln Phe Leu Gly Gly Leu Leu Ile Gly Ala Gly
     125     130     135
Cys Ala Leu Tyr Pro Leu Gly Trp Asp Ser Glu Glu Val Arg Gln
     140     145     150
Thr Cys Gly Tyr Thr Ser Gly Gln Phe Asp Leu Gly Lys Cys Glu
     155     160     165
Ile Gly Trp Ala Tyr Tyr Cys Thr Gly Ala Gly Ala Thr Ala Ala
     170     175     180
Met Leu Leu Cys Thr Trp Leu Ala Cys Phe Ser Gly Lys Lys Gln
     185     190     195
Lys His Tyr Pro Tyr
      200

```

<210> 114

<211> 225

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2093492

<400> 114

```

Met Gly Phe Arg Leu Glu Gly Ile Phe Pro Ala Ala Leu Leu Pro
 1          5          10          15
Leu Leu Leu Thr Met Ile Leu Phe Leu Gly Pro Leu Met Gln Leu
 20          25          30
Ser Met Asp Cys Pro Cys Asp Leu Ala Asp Gly Leu Lys Val Val
 35          40          45
Leu Ala Pro Arg Ser Trp Ala Arg Cys Leu Thr Asp Met Arg Trp
 50          55          60
Leu Arg Asn Gln Val Ile Ala Pro Leu Thr Glu Glu Leu Val Phe
 65          70          75
Arg Ala Cys Met Leu Pro Met Leu Ala Pro Cys Met Gly Leu Gly
 80          85          90
Pro Ala Val Phe Thr Cys Pro Leu Phe Phe Gly Val Ala His Phe
 95          100         105
His His Ile Ile Glu Gln Leu Arg Phe Arg Gln Ser Ser Val Gly
 110         115         120
Asn Ile Phe Leu Ser Ala Ala Phe Gln Phe Ser Tyr Thr Ala Val
 125         130         135
Phe Gly Ala Tyr Thr Ala Phe Leu Phe Ile Arg Thr Gly His Leu
 140         145         150
Ile Gly Pro Val Leu Cys His Ser Phe Cys Asn Tyr Met Gly Phe
 155         160         165
Pro Ala Val Cys Ala Ala Leu Glu His Pro Gln Arg Arg Pro Leu
 170         175         180
Leu Ala Gly Tyr Ala Leu Gly Val Gly Leu Phe Leu Leu Leu Leu
 185         190         195
Gln Pro Leu Thr Asp Pro Lys Leu Tyr Gly Ser Leu Pro Leu Cys
 200         205         210
Val Leu Leu Glu Arg Ala Gly Asp Ser Glu Ala Pro Leu Cys Ser
 215         220         225

```

<210> 115

<211> 155

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2108789

<400> 115

```

Met Ser Gly Leu Leu Ile Pro Pro Leu Pro Gly Trp Val Leu Gly
 1          5          10          15
Pro Leu Met Trp Ala Cys Arg Pro Pro Gln Asp Glu Pro Ser Gly
 20          25          30

```

```

Thr Asp Pro Pro Pro Pro Arg Leu Gln Pro His His Val Ser Gly
      35                                40                                45
Leu Gly Leu Gly Gln Ala Trp Ala Gln Ser Trp Ala Pro Arg Gly
      50                                55                                60
Ser Pro Pro Leu Thr Trp Leu Leu Pro Thr Leu Pro Leu Lys Asp
      65                                70                                75
Gly Pro Ala Ala Arg Leu Pro Pro Pro Pro His Thr Thr Leu Gly
      80                                85                                90
Gly Leu Ser His Pro Pro Gln Pro Arg Ser Ala Gln Thr Asp Pro
      95                                100                               105
His Ser Ile Pro Arg Pro Ala Ala Gln Val Arg Gly Pro Val Leu
     110                               115                               120
Pro Gly Ala Trp Ala Thr Pro Tyr Ala Ile Ser Ser Glu Gln Pro
     125                               130                               135
Gly Pro Thr Asp Pro His Ala Leu Ser Tyr Val Pro Phe Ser Pro
     140                               145                               150
Asp Phe Phe Cys Thr
      155

```

<210> 116

<211> 468

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2171401

<400> 116

```

Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
  1      5      10      15
Trp Leu Leu Ser Ser Gly His Gly Glu Gln Pro Pro Glu Thr
     20      25      30
Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp
     35      40      45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg
     50      55      60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg
     65      70      75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp
     80      85      90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln
     95     100     105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr
    110     115     120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu
    125     130     135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys
    140     145     150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe
    155     160     165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp
    170     175     180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp

```


	185		190		195
Ala Trp Lys Ile	Trp Asn Val Ile Tyr	Glu Glu Asn Cys Phe	Lys		
	200		205		210
Pro Gln Thr Ile	Lys Arg Pro Leu Asn	Pro Leu Ala Ser Gly	Gln		
	215		220		225
Gly Thr Ser Glu	Glu Asn Thr Phe Tyr	Ser Trp Leu Glu Gly	Leu		
	230		235		240
Cys Val Glu Lys	Arg Ala Phe Tyr Arg	Leu Ile Ser Gly Leu	His		
	245		250		255
Ala Ser Ile Asn	Val His Leu Ser Ala	Arg Tyr Leu Leu Gln	Glu		
	260		265		270
Thr Trp Leu Glu	Lys Lys Trp Gly His	Asn Ile Thr Glu Phe	Gln		
	275		280		285
Gln Arg Phe Asp	Gly Ile Leu Thr Glu	Gly Glu Gly Pro Arg	Arg		
	290		295		300
Leu Lys Asn Leu	Tyr Phe Leu Tyr Leu	Ile Glu Leu Arg Ala	Leu		
	305		310		315
Ser Lys Val Leu	Pro Phe Phe Glu Arg	Pro Asp Phe Gln Leu	Phe		
	320		325		330
Thr Gly Asn Lys	Ile Gln Asp Glu Glu	Asn Lys Met Leu Leu	Leu		
	335		340		345
Glu Ile Leu His	Glu Ile Lys Ser Phe	Pro Leu His Phe Asp	Glu		
	350		355		360
Asn Ser Phe Phe	Ala Gly Asp Lys Lys	Glu Ala His Lys Leu	Lys		
	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met	Asp		
	380		385		390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln	Thr		
	395		400		405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys	Leu		
	410		415		420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His	Leu		
	425		430		435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg	Ile		
	440		445		450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu	Gln		
	455		460		465
Asn Ile His					

<210> 117

<211> 403

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2212530

<400> 117

Met Ser Thr Ser	Thr Ser Pro Ala	Ala Met Leu Leu	Arg Arg Leu
1	5	10	15
Arg Arg Leu Ser	Trp Gly Ser Thr	Ala Val Gln Leu	Phe Ile Leu
	20	25	30
Thr Val Val Thr	Phe Gly Leu Leu	Ala Pro Leu	Ala Cys His Arg

	35		40		45
Leu Leu His Ser Tyr Phe Tyr Leu Arg His Trp His Leu Asn Gln					
	50		55		60
Met Ser Gln Glu Phe Leu Gln Gln Ser Leu Lys Glu Gly Glu Ala					
	65		70		75
Ala Leu His Tyr Phe Glu Glu Leu Pro Ser Ala Asn Gly Ser Val					
	80		85		90
Pro Ile Val Trp Gln Ala Thr Pro Arg Pro Trp Leu Val Ile Thr					
	95		100		105
Ile Ile Thr Val Asp Arg Gln Pro Gly Phe His Tyr Val Leu Gln					
	110		115		120
Val Val Ser Gln Phe His Arg Leu Leu Gln Gln Cys Gly Pro Gln					
	125		130		135
Cys Glu Gly His Gln Leu Phe Leu Cys Asn Val Glu Arg Ser Val					
	140		145		150
Ser His Phe Asp Ala Lys Leu Leu Ser Lys Tyr Val Pro Val Ala					
	155		160		165
Asn Arg Tyr Glu Gly Thr Glu Asp Asp Tyr Gly Asp Asp Pro Ser					
	170		175		180
Thr Asn Ser Phe Glu Lys Glu Lys Gln Asp Tyr Val Tyr Cys Leu					
	185		190		195
Glu Ser Ser Leu Gln Thr Tyr Asn Pro Asp Tyr Val Leu Met Val					
	200		205		210
Glu Asp Asp Ala Val Pro Glu Glu Gln Ile Phe Pro Val Leu Glu					
	215		220		225
His Leu Leu Arg Ala Arg Phe Ser Glu Pro His Leu Arg Asp Ala					
	230		235		240
Leu Tyr Leu Lys Leu Tyr His Pro Glu Arg Leu Gln His Tyr Ile					
	245		250		255
Asn Pro Glu Pro Met Arg Ile Leu Glu Trp Val Gly Val Gly Met					
	260		265		270
Leu Leu Gly Pro Leu Leu Thr Trp Ile Tyr Met Arg Phe Ala Ser					
	275		280		285
Arg Pro Gly Phe Ser Trp Pro Val Met Leu Phe Phe Ser Leu Tyr					
	290		295		300
Ser Met Gly Leu Val Glu Leu Val Gly Arg His Tyr Phe Leu Glu					
	305		310		315
Leu Arg Arg Leu Ser Pro Ser Leu Tyr Ser Val Val Pro Ala Ser					
	320		325		330
Gln Cys Cys Thr Pro Ala Met Leu Phe Pro Ala Pro Ala Ala Arg					
	335		340		345
Arg Thr Leu Thr Tyr Leu Ser Gln Val Tyr Cys His Lys Gly Phe					
	350		355		360
Gly Lys Asp Met Ala Leu Tyr Ser Leu Leu Arg Ala Lys Gly Glu					
	365		370		375
Arg Ala Tyr Val Val Glu Pro Asn Leu Val Lys His Ile Gly Leu					
	380		385		390
Phe Ser Ser Leu Arg Tyr Asn Phe His Pro Ser Leu Leu					
	395		400		

<210> 118

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2253036

<400> 118

```

Met Glu Arg Cys Phe His Cys Phe Pro Val His Leu Val Phe Asn
 1          5          10          15
Leu Val Gln Ser Phe Ser Pro Ile Ser Gly Val Glu Ser Cys Leu
          20          25          30
Leu Pro Gln Cys Asp Lys Cys Trp Pro Met Val Tyr Arg Ser Cys
          35          40          45
Asp Ala Ser Arg Gly Leu Val Asn Ala Cys Ile Leu Gly Phe Val
          50          55          60
Leu Leu Glu Cys Ser Phe Val Gly Ala Leu Asn Asn Tyr Val Arg
          65          70          75
Ser Leu Ala Thr Leu Leu Glu Arg Thr His Gly Gly Lys Arg Leu
          80          85          90
Lys Leu Cys Glu Glu Ser Gln Ala Ser His Pro Ser Phe Ser Ala
          95          100          105
Glu Pro Arg His Gln Pro Thr Cys Gln Leu Asn Ala Thr Val Arg
          110          115          120
Val Ile Thr Ser Lys Ile Thr Arg Lys Thr Thr
          125          130

```

<210> 119

<211> 556

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2280161

<400> 119

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu
 1          5          10          15
Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly
          20          25          30
Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro
          35          40          45
Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe
          50          55          60
Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp
          65          70          75
Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr
          80          85          90
Asn Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu Tyr Leu
          95          100          105
Glu Lys Leu Lys Glu Lys Arg Gly Leu Ser Gly Lys Tyr Gln Thr
          110          115          120
Ser Ser Lys Leu Phe Gln Asn Cys Ser Glu Leu Phe Lys Thr Gln
          125          130          135
Thr Phe Ser Gly Asp Phe Met His Arg Leu Pro Leu Leu Gly Glu
          140          145          150

```

Lys	Gln	Glu	Ala	Lys	Glu	Asn	Gly	Thr	Asn	Leu	Thr	Phe	Ile	Gly	
				155					160					165	
Asp	Lys	Thr	Ala	Met	His	Glu	Pro	Leu	Gln	Thr	Trp	Gln	Asp	Ala	
				170					175					180	
Pro	Tyr	Ile	Phe	Ile	Val	His	Ile	Gly	Ile	Ser	Ser	Ser	Lys	Glu	
				185					190					195	
Ser	Ser	Lys	Glu	Asn	Ser	Leu	Ser	Asn	Leu	Phe	Thr	Met	Thr	Val	
				200					205					210	
Glu	Val	Lys	Gly	Pro	Tyr	Glu	Tyr	Leu	Thr	Leu	Glu	Asp	Tyr	Pro	
				215					220					225	
Leu	Met	Ile	Phe	Phe	Met	Val	Met	Cys	Ile	Val	Tyr	Val	Leu	Phe	
				230					235					240	
Gly	Val	Leu	Trp	Leu	Ala	Trp	Ser	Ala	Cys	Tyr	Trp	Arg	Asp	Leu	
				245					250					255	
Leu	Arg	Ile	Gln	Phe	Trp	Ile	Gly	Ala	Val	Ile	Phe	Leu	Gly	Met	
				260					265					270	
Leu	Glu	Lys	Ala	Val	Phe	Tyr	Ala	Glu	Phe	Gln	Asn	Ile	Arg	Tyr	
				275					280					285	
Lys	Gly	Glu	Ser	Val	Gln	Gly	Ala	Leu	Ile	Leu	Ala	Glu	Leu	Leu	
				290					295					300	
Ser	Ala	Val	Lys	Arg	Ser	Leu	Ala	Arg	Thr	Leu	Val	Ile	Ile	Val	
				305					310					315	
Ser	Leu	Gly	Tyr	Gly	Ile	Val	Lys	Pro	Arg	Leu	Gly	Val	Thr	Leu	
				320					325					330	
His	Lys	Val	Val	Val	Ala	Gly	Ala	Leu	Tyr	Leu	Leu	Phe	Ser	Gly	
				335					340					345	
Met	Glu	Gly	Val	Leu	Arg	Val	Thr	Gly	Tyr	Phe	Ser	Tyr	Pro	Leu	
				350					355					360	
Thr	Leu	Ile	Val	Asn	Leu	Ala	Leu	Ser	Ala	Val	Asp	Ala	Cys	Val	
				365					370					375	
Ile	Leu	Trp	Ile	Phe	Ile	Ser	Leu	Thr	Gln	Thr	Met	Lys	Leu	Leu	
				380					385					390	
Lys	Leu	Arg	Arg	Asn	Ile	Val	Lys	Leu	Ser	Leu	Tyr	Arg	His	Phe	
				395					400					405	
Thr	Asn	Thr	Leu	Ile	Leu	Ala	Val	Ala	Ala	Ser	Ile	Val	Phe	Ile	
				410					415					420	
Ile	Trp	Thr	Thr	Met	Lys	Phe	Arg	Ile	Val	Thr	Cys	Gln	Ser	Asp	
				425					430					435	
Trp	Arg	Glu	Leu	Trp	Val	Asp	Asp	Ala	Ile	Trp	Arg	Leu	Leu	Phe	
				440					445					450	
Ser	Met	Ile	Leu	Phe	Val	Ile	Met	Val	Leu	Trp	Arg	Pro	Ser	Ala	
				455					460					465	
Asn	Asn	Gln	Arg	Phe	Ala	Phe	Ser	Pro	Leu	Ser	Glu	Glu	Glu	Glu	
				470					475					480	
Glu	Asp	Glu	Gln	Lys	Glu	Pro	Met	Leu	Lys	Glu	Ser	Phe	Glu	Gly	
				485					490					495	
Met	Lys	Met	Arg	Ser	Thr	Lys	Gln	Glu	Pro	Asn	Gly	Asn	Ser	Lys	
				500					505					510	
Val	Asn	Lys	Ala	Gln	Glu	Asp	Asp	Leu	Lys	Trp	Val	Glu	Glu	Asn	
				515					520					525	
Val	Pro	Ser	Ser	Val	Thr	Asp	Val	Ala	Leu	Pro	Ala	Leu	Leu	Asp	
				530					535					540	
Ser	Asp	Glu	Glu	Arg	Met	Ile	Thr	His	Phe	Glu	Arg	Ser	Lys	Met	
				545					550					555	
Glu															

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<220>  
<221> misc_feature  
<223> Incyte Clone No: 2287485
```

79/167

```

Arg Tyr Ser Arg Gly Val Leu Ser Ser Arg Val Met Gly Gly Thr
      350                      355                      360
Glu Phe Val Phe Lys Val Asn His Met Lys Val Thr Pro Met Asp
      365                      370                      375
Ala Ala Thr Ala Ser Leu Leu Asn Val Phe Asn Gly Asn Glu Cys
      380                      385                      390
Gly Ala Glu Gly Ser Trp Gln Val Gly Ile Gln Gln Asp Val Thr
      395                      400                      405
His Thr Asn Gly Cys Val Ala Leu Gly Ile Lys Leu Pro His Thr
      410                      415                      420
Glu Tyr Glu Ile Phe Lys Met Glu Gln Asp Ala Arg Gly Arg Tyr
      425                      430                      435
Leu Leu Phe Asn Gly Gln Arg Pro Ser Asp Gly Ser Ser Pro Asp
      440                      445                      450
Arg Pro Glu Lys Arg Ala Thr Ser Tyr Gln Met Pro Leu Val Gln
      455                      460                      465
Cys Ala Ser Ser Ser Pro Arg Ala Glu Asp Leu Ala Glu Asp Ser
      470                      475                      480
Gly Ser Ser Leu Tyr Gly Arg Ala Pro Gly Arg His Thr Trp Ser
      485                      490                      495
Leu Leu Leu Ala Ala Leu Ala Cys Leu Val Pro Leu Leu His Trp
      500                      505                      510
Asn Ile Arg Arg

```

<210> 121

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2380344

<400> 121

```

Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
  1                      5                      10                      15
Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
      20                      25                      30
Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
      35                      40                      45
Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
      50                      55                      60
Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
      65                      70                      75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
      80                      85                      90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
      95                      100                     105
Arg Arg Arg Asp

```

<210> 122

<211> 431
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2383171

<400> 122

Met	Ser	Trp	Val	Gln	Ala	Thr	Leu	Leu	Ala	Arg	Gly	Leu	Cys	Arg	1	5	10	15
Ala	Trp	Gly	Gly	Thr	Cys	Gly	Ala	Ala	Leu	Thr	Gly	Thr	Ser	Ile	20	25	30	35
Ser	Gln	Val	Pro	Arg	Arg	Leu	Pro	Arg	Gly	Leu	His	Cys	Ser	Ala	40	45	50	55
Ala	Ala	His	Ser	Ser	Glu	Gln	Ser	Leu	Val	Pro	Ser	Pro	Pro	Glu	60	65	70	75
Pro	Arg	Gln	Arg	Pro	Thr	Lys	Ala	Leu	Val	Pro	Phe	Glu	Asp	Leu	80	85	90	95
Gln	Thr	Val	Gln	Lys	Phe	Ala	Glu	His	Ser	Val	Arg	Lys	Arg	Gly	100	105	110	115
His	Ile	Asp	Phe	Ile	Tyr	Leu	Ala	Leu	Arg	Lys	Met	Arg	Glu	Tyr	120	125	130	135
Gly	Val	Glu	Arg	Asp	Leu	Ala	Val	Tyr	Asn	Gln	Leu	Leu	Asn	Ile	140	145	150	155
Phe	Pro	Lys	Glu	Val	Phe	Arg	Pro	Arg	Asn	Ile	Ile	Gln	Arg	Ile	160	165	170	175
Phe	Val	His	Tyr	Pro	Arg	Gln	Gln	Glu	Cys	Gly	Ile	Ala	Val	Leu	180	185	190	195
Glu	Gln	Met	Glu	Asn	His	Gly	Val	Met	Pro	Asn	Lys	Glu	Thr	Glu	200	205	210	215
Phe	Leu	Leu	Ile	Gln	Ile	Phe	Gly	Arg	Lys	Ser	Tyr	Pro	Met	Leu	220	225	230	235
Lys	Leu	Val	Arg	Leu	Lys	Leu	Trp	Phe	Pro	Arg	Phe	Met	Asn	Val	240	245	250	255
Asn	Pro	Phe	Pro	Val	Pro	Arg	Asp	Leu	Pro	Gln	Asp	Pro	Val	Glu	260	265	270	275
Leu	Ala	Met	Phe	Gly	Leu	Arg	His	Met	Glu	Pro	Asp	Leu	Ser	Ala	280	285	290	295
Arg	Val	Thr	Ile	Tyr	Gln	Val	Pro	Leu	Pro	Lys	Asp	Ser	Thr	Gly	300	305	310	315
Ala	Ala	Asp	Pro	Pro	Gln	Pro	His	Ile	Val	Gly	Ile	Gln	Ser	Pro	320	325	330	335
Asp	Gln	Gln	Ala	Ala	Leu	Ala	Arg	His	Asn	Pro	Ala	Arg	Pro	Val	340	345	350	355
Phe	Val	Glu	Gly	Pro	Phe	Ser	Leu	Trp	Leu	Arg	Asn	Lys	Cys	Val				
Tyr	Tyr	His	Ile	Leu	Arg	Ala	Asp	Leu	Leu	Pro	Pro	Glu	Glu	Arg				
Glu	Val	Glu	Glu	Thr	Pro	Glu	Glu	Trp	Asn	Leu	Tyr	Tyr	Pro	Met				
Gln	Leu	Asp	Leu	Glu	Tyr	Val	Arg	Ser	Gly	Trp	Asp	Asn	Tyr	Glu				
Phe	Asp	Ile	Asn	Glu	Val	Glu	Glu	Gly	Pro	Val	Phe	Ala	Met	Cys				

Met	Ala	Gly	Ala	His	Asp	Gln	Ala	Thr	Met	Ala	Lys	Trp	Ile	Gln	
				365					370					375	
Gly	Leu	Gln	Glu	Thr	Asn	Pro	Thr	Leu	Ala	Gln	Ile	Pro	Val	Val	
				380					385					390	
Phe	Arg	Leu	Ala	Gly	Ser	Thr	Arg	Glu	Leu	Gln	Thr	Ser	Ser	Ala	
				395					400					405	
Gly	Leu	Glu	Glu	Pro	Pro	Leu	Pro	Glu	Asp	His	Gln	Glu	Glu	Asp	
				410					415					420	
Asp	Asn	Leu	Gln	Arg	Gln	Gln	Gln	Gly	Gln	Ser					
				425					430						

<210> 123
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2396046

<400> 123

Met	Leu	Leu	Gly	Val	Arg	Ala	Val	Pro	Leu	Cys	Ser	Ala	Trp	Gln	
1				5					10					15	
Gly	Ala	Val	Gly	Leu	Val	Ser	Leu	Ala	Ile	Ser	Ile	Cys	Lys	His	
				20					25					30	
Gly	Leu	Ser	Ser	Gln	Gln	Asn	Leu	Val	Pro	Gly	Lys	Ser	Asn	Val	
				35					40					45	
Pro	Lys	Ala	Ser	Asp	Met	Pro	Arg	Cys	Pro	Pro	Val	Phe	Gln	Ser	
				50					55					60	
Pro	Asn	Leu	Thr	Pro	Phe	Pro	His	His	Thr	Lys	His	Thr	Ser	Gln	
				65					70					75	
Gly	Ser	His	Leu	Gly	Val	Pro	Pro	Pro	Ala	Pro	Met	Pro	Trp	Cys	
				80					85					90	
Pro	Gln	Ala	Gln	Gly	Phe	Gly	Leu	Ser	Cys	Gln	Ser	Leu	Asp	Ala	
				95					100					105	
Phe	Glu	Gly	Gln	Leu	Gly	Cys	Gly	Trp	Gly	Val	Gln	Ala	Ala	Gly	
				110					115					120	
Glu	Pro	Arg	Leu	Arg	Ile	Ile	His	Thr	Leu	Leu	Phe	Gly	Ala	Phe	
				125					130					135	
Val	Glu	Val	Ser	Arg	Ile	Pro									
				140											

<210> 124
 <211> 643
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2456587

<400> 124

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15
Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp
			140						145					150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln
			155						160					165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly
			170						175					180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln
			185						190					195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Ile	Pro	Tyr
			200						205					210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu
			215						220					225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser
			230						235					240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp
			245						250					255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro
			260						265					270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala
			275						280					285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg
			290						295					300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly
			305						310					315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn
			320						325					330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile
			335						340					345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro
			350						355					360
Ala	Ser	Asp	Gly	Tyr	Lys	Gln	Ile	Met	Pro	Tyr	Asp	Leu	Tyr	His
			365						370					375
Pro	Leu	Pro	Arg	Trp	Glu	Ala	Thr	Pro	Trp	Thr	Ala	Cys	Ser	Ser
			380						385					390
Ser	Cys	Gly	Gly	Gly	Ile	Gln	Ser	Arg	Ala	Val	Ser	Cys	Val	Glu
			395						400					405
Glu	Asp	Ile	Gln	Gly	His	Val	Thr	Ser	Val	Glu	Glu	Trp	Lys	Cys
			410						415					420

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Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe
      425                      430                      435
Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val
      440                      445                      450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp
      455                      460                      465
His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro
      470                      475                      480
His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro
      485                      490                      495
Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln
      500                      505                      510
Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser
      515                      520                      525
Phe Ile Pro Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val
      530                      535                      540
Gly Thr Gln Val Arg Ile Val Arg Cys Gln Val Leu Leu Ser Phe
      545                      550                      555
Ser Gln Ser Val Ala Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro
      560                      565                      570
Lys Pro Ala Ser Gln Arg Ala Cys Tyr Ala Gly Pro Cys Ser Gly
      575                      580                      585
Glu Ile Pro Glu Phe Asn Pro Asp Glu Thr Asp Gly Leu Phe Gly
      590                      595                      600
Gly Leu Gln Asp Phe Asp Glu Leu Tyr Asp Trp Glu Tyr Glu Gly
      605                      610                      615
Phe Thr Lys Cys Ser Glu Ser Cys Gly Gly Gly Val Gln Glu Ala
      620                      625                      630
Val Val Ser Cys Leu Asn Lys Gln Thr Arg Glu Pro Cys
      635                      640

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<210> 125

<211> 568

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2484813

<400> 125

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Met Val Leu Leu His Trp Cys Leu Leu Trp Leu Leu Phe Pro Leu
  1                      5                      10                      15
Ser Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe
      20                      25                      30
Gln Met Gln Ile Arg Asp Lys Ala Phe Phe His Asp Ser Ser Val
      35                      40                      45
Ile Pro Asp Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr
      50                      55                      60
Pro Lys Arg Tyr Phe Phe Val Val Glu Glu Asp Asn Thr Pro Leu
      65                      70                      75
Ser Val Thr Val Thr Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu
      80                      85                      90
Ser Leu Gln Glu Leu Pro Glu Asp Arg Ser Gly Glu Gly Ser Gly

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	95		100		105
Asp Leu Glu Pro	Leu Glu Gln Gln Lys	Gln Gln Ile Ile Asn	Glu		
	110		115		120
Glu Gly Thr Glu	Leu Phe Ser Tyr Lys	Gly Asn Asp Val Glu	Tyr		
	125		130		135
Phe Ile Ser Ser	Ser Ser Pro Ser Gly	Leu Tyr Gln Leu Asp	Leu		
	140		145		150
Leu Ser Thr Glu	Lys Asp Thr His Phe	Lys Val Tyr Ala Thr	Thr		
	155		160		165
Thr Pro Glu Ser	Asp Gln Pro Tyr Pro	Glu Leu Pro Tyr Asp	Pro		
	170		175		180
Arg Val Asp Val	Thr Ser Leu Gly Arg	Thr Thr Val Thr Leu	Ala		
	185		190		195
Trp Lys Pro Ser	Pro Thr Ala Ser Leu	Leu Lys Gln Pro Ile	Gln		
	200		205		210
Tyr Cys Val Val	Ile Asn Lys Glu His	Asn Phe Lys Ser Leu	Cys		
	215		220		225
Ala Val Glu Ala	Lys Leu Ser Ala Asp	Asp Ala Phe Met Met	Ala		
	230		235		240
Pro Lys Pro Gly	Leu Asp Phe Ser Pro	Phe Asp Phe Ala His	Phe		
	245		250		255
Gly Phe Pro Ser	Asp Asn Ser Gly Lys	Glu Arg Ser Phe Gln	Ala		
	260		265		270
Lys Pro Ser Pro	Lys Leu Gly Arg His	Val Tyr Ser Arg Pro	Lys		
	275		280		285
Val Asp Ile Gln	Lys Ile Cys Ile Gly	Asn Lys Asn Ile Phe	Thr		
	290		295		300
Val Ser Asp Leu	Lys Pro Asp Thr Gln	Tyr Tyr Phe Asp Val	Phe		
	305		310		315
Val Val Asn Ile	Asn Ser Asn Met Ser	Thr Ala Tyr Val Gly	Thr		
	320		325		330
Phe Ala Arg Thr	Lys Glu Glu Ala Lys	Gln Lys Thr Val Glu	Leu		
	335		340		345
Lys Asp Gly Lys	Ile Thr Asp Val Phe	Val Lys Arg Lys Gly	Ala		
	350		355		360
Lys Phe Leu Arg	Phe Ala Pro Val Ser	Ser His Gln Lys Val	Thr		
	365		370		375
Phe Phe Ile His	Ser Cys Leu Asp Ala	Val Gln Ile Gln Val	Arg		
	380		385		390
Arg Asp Gly Lys	Leu Leu Leu Ser Gln	Asn Val Glu Gly Ile	Gln		
	395		400		405
Gln Phe Gln Leu	Arg Gly Lys Pro Lys	Ala Lys Tyr Leu Val	Arg		
	410		415		420
Leu Lys Gly Asn	Lys Lys Gly Ala Ser	Met Leu Lys Ile Leu	Ala		
	425		430		435
Thr Thr Arg Pro	Thr Lys Gln Ser Phe	Pro Ser Leu Pro Glu	Asp		
	440		445		450
Thr Arg Ile Lys	Ala Phe Asp Lys Leu	Arg Thr Cys Ser Ser	Ala		
	455		460		465
Thr Val Ala Trp	Leu Gly Thr Gln Glu	Arg Asn Lys Phe Cys	Ile		
	470		475		480
Tyr Lys Lys Glu	Val Asp Asp Asn Tyr	Asn Glu Asp Gln Lys	Lys		
	485		490		495
Arg Glu Gln Asn	Gln Cys Leu Gly Pro	Asp Ile Arg Lys Lys	Ser		
	500		505		510
Glu Lys Val Leu	Cys Lys Tyr Phe His	Ser Gln Asn Leu Gln	Lys		
	515		520		525

Ala Val Thr Thr Glu Thr Ile Lys Gly Leu Gln Pro Gly Lys Ser
 530 535 540
 Tyr Leu Leu Asp Val Tyr Val Ile Gly His Gly Gly His Ser Val
 545 550 555
 Lys Tyr Gln Ser Lys Val Val Lys Thr Arg Lys Phe Cys
 560 565

<210> 126
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2493851

<400> 126
 Met Trp Leu Val Gly Pro Ser Phe Leu Ser Cys Pro Leu Gly Lys
 1 5 10 15
 Val Pro Pro Ala Gly Leu Leu Leu Ala Gly Ser Ser Gly Arg Gly
 20 25 30
 Ala Arg Arg Pro Ala Thr Pro Arg His Trp Ser Ser Thr Thr Pro
 35 40 45
 Gly Leu Arg Leu Glu Ala Pro Leu Cys Gln Leu Cys Pro Leu Gly
 50 55 60
 Gly Thr Arg Gln Asp Cys Gln Pro Leu Ser Trp Gln Val Thr Ser
 65 70 75
 Ala Phe Lys Leu Thr Val Pro Ser Pro Phe His Ala Pro Pro Arg
 80 85 90
 Ser Trp Ser Cys Leu Leu Leu Gly Ile Phe Pro Gly Gln Ala Leu
 95 100 105
 Ala Leu Glu Pro Trp His Leu Phe Leu Gly Ser Met Leu Pro Arg
 110 115 120
 Cys Asp Gly Glu Cys
 125

<210> 127
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2495719

<400> 127
 Met Ala Ala Leu Lys Ala Leu Val Ser Gly Cys Gly Arg Leu Leu
 1 5 10 15
 Arg Gly Leu Leu Ala Gly Pro Ala Ala Thr Ser Trp Ser Arg Leu
 20 25 30
 Pro Ala Arg Gly Phe Arg Glu Val Val Glu Thr Gln Glu Gly Lys

	35		40		45
Thr Thr Ile Ile Glu Gly Arg Ile Thr Ala Thr Pro Lys Glu Ser					
	50		55		60
Pro Asn Pro Pro Asn Pro Ser Gly Gln Cys Pro Ile Cys Arg Trp					
	65		70		75
Asn Leu Lys His Lys Tyr Asn Tyr Asp Asp Val Leu Leu Leu Ser					
	80		85		90
Gln Phe Ile Arg Pro His Gly Gly Met Leu Pro Arg Lys Ile Thr					
	95		100		105
Gly Leu Cys Gln Glu His Arg Lys Ile Glu Glu Cys Val Lys					
	110		115		120
Met Ala His Arg Ala Gly Leu Leu Pro Asn His Arg Pro Arg Leu					
	125		130		135
Pro Glu Gly Val Val Pro Lys Ser Lys Pro Gln Leu Asn Arg Tyr					
	140		145		150
Leu Thr Arg Trp Ala Pro Gly Ser Val Lys Pro Ile Tyr Lys Lys					
	155		160		165
Gly Pro Arg Trp Asn Arg Val Arg Met Pro Val Gly Ser Pro Leu					
	170		175		180
Leu Arg Asp Asn Val Cys Tyr Ser Arg Thr Pro Trp Lys Leu Tyr					
	185		190		195
His					

<210> 128

<211> 214

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2614153

<400> 128

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly					
1	5		10		15
Gln Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val					
	20		25		30
Ser Arg Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr					
	35		40		45
Ser Ala Gly Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser					
	50		55		60
Trp Glu Tyr Gly Asp Pro His Ser Pro Val Ile Leu Cys Ser Tyr					
	65		70		75
Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro Val Asp His Val					
	80		85		90
Gly Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly Cys Leu Lys					
	95		100		105
Phe Gly Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser Val Gln					
	110		115		120
Cys His Ala Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr Phe					
	125		130		135
Leu Arg Glu Asn Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe					
	140		145		150
Ile Thr Thr Leu Leu Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val					

	155		160		165
Asp Arg Phe Cys	Leu Gly His Thr Gly	Thr Ala Val Gly Lys	Leu		
	170		175		180
Leu Thr Leu Gly	Gly Leu Gly Ile Trp	Trp Phe Val Asp Leu	Ile		
	185		190		195
Leu Leu Ile Thr	Gly Gly Leu Met Pro	Ser Asp Gly Ser Asn	Trp		
	200		205		210
Cys Thr Val Tyr					

<210> 129
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2655184

<400> 129	
Met Ala Cys Phe Ser Phe Phe Leu Cys Phe Leu Val His Leu Leu	
1 5 10 15	
Ile Lys Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser	
20 25 30	
Pro Pro Ser Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala	
35 40 45	
Ser Cys Asp Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Val Ser	
50 55 60	
His Asp Pro Gly Trp Pro Val Val Arg Leu His Arg Pro Leu Val	
65 70 75	
Pro Glu His Ala Val Phe Ser Gln Pro Ser Leu Gln Pro	
80 85	

<210> 130
 <211> 260
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2848362

<400> 130	
Met Pro Asp Pro Leu Phe Ser Ala Val Gln Gly Lys Asp Glu Ile	
1 5 10 15	
Leu His Lys Ala Leu Cys Phe Cys Pro Trp Leu Gly Lys Gly Gly	
20 25 30	
Met Glu Pro Leu Arg Leu Leu Ile Leu Leu Phe Val Thr Glu Leu	
35 40 45	
Ser Gly Ala His Asn Thr Thr Val Phe Gln Gly Val Ala Gly Gln	
50 55 60	
Ser Leu Gln Val Ser Cys Pro Tyr Asp Ser Met Lys His Trp Gly	

	65		70		75
Arg Arg Lys Ala Trp Cys Arg Gln Leu Gly Glu Lys Gly Pro Cys					
	80		85		90
Gln Arg Val Val Ser Thr His Asn Leu Trp Leu Leu Ser Phe Leu					
	95		100		105
Arg Arg Trp Asn Gly Ser Thr Ala Ile Thr Asp Asp Thr Leu Gly					
	110		115		120
Gly Thr Leu Thr Ile Thr Leu Arg Asn Leu Gln Pro His Asp Ala					
	125		130		135
Gly Leu Tyr Gln Cys Gln Ser Leu His Gly Ser Glu Ala Asp Thr					
	140		145		150
Leu Arg Lys Val Leu Val Glu Val Leu Ala Asp Pro Leu Asp His					
	155		160		165
Arg Asp Ala Gly Asp Leu Trp Phe Pro Gly Glu Ser Glu Ser Phe					
	170		175		180
Glu Asp Ala His Val Glu His Ser Ile Ser Arg Ser Leu Leu Glu					
	185		190		195
Gly Glu Ile Pro Phe Pro Pro Thr Ser Ile Leu Leu Leu Leu Ala					
	200		205		210
Cys Ile Phe Leu Ile Lys Ile Leu Ala Ala Ser Ala Leu Trp Ala					
	215		220		225
Ala Ala Trp His Gly Gln Lys Pro Gly Thr His Pro Pro Ser Glu					
	230		235		240
Leu Asp Cys Gly His Asp Pro Gly Tyr Gln Leu Gln Thr Leu Pro					
	245		250		255
Gly Leu Arg Asp Thr					
	260				

<210> 131

<211> 295

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2849906

<400> 131

Met Gly Leu Pro Val Ser Trp Ala Pro Pro Ala Leu Trp Val Leu					
1	5		10		15
Gly Cys Cys Ala Leu Leu Leu Ser Leu Trp Ala Leu Cys Thr Ala					
	20		25		30
Cys Arg Arg Pro Glu Asp Ala Val Ala Pro Arg Lys Arg Ala Arg					
	35		40		45
Arg Gln Arg Ala Arg Leu Gln Gly Ser Ala Thr Ala Ala Glu Ala					
	50		55		60
Ser Leu Leu Arg Arg Thr His Leu Cys Ser Leu Ser Lys Ser Asp					
	65		70		75
Thr Arg Leu His Glu Leu His Arg Gly Pro Arg Ser Ser Arg Ala					
	80		85		90
Leu Arg Pro Ala Ser Met Asp Leu Leu Arg Pro His Trp Leu Glu					
	95		100		105
Val Ser Arg Asp Ile Thr Gly Pro Gln Ala Ala Pro Ser Ala Phe					
	110		115		120

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Pro His Gln Glu Leu Pro Arg Ala Leu Pro Ala Ala Ala Ala Thr
125 130 135
Ala Gly Cys Ala Gly Leu Glu Ala Thr Tyr Ser Asn Val Gly Leu
140 145 150
Ala Ala Leu Pro Gly Val Ser Leu Ala Ala Ser Pro Val Val Ala
155 160 165
Glu Tyr Ala Arg Val Gln Lys Arg Lys Gly Thr His Arg Ser Pro
170 175 180
Gln Glu Pro Gln Gln Gly Lys Thr Glu Val Thr Pro Ala Ala Gln
185 190 195
Val Asp Val Leu Tyr Ser Arg Val Cys Lys Pro Lys Arg Arg Asp
200 205 210
Pro Gly Pro Thr Thr Asp Pro Leu Asp Pro Lys Gly Gln Gly Ala
215 220 225
Ile Leu Ala Leu Ala Gly Asp Leu Ala Tyr Gln Thr Leu Pro Leu
230 235 240
Arg Ala Leu Asp Val Asp Ser Gly Pro Leu Glu Asn Val Tyr Glu
245 250 255
Ser Ile Arg Glu Leu Gly Asp Pro Ala Gly Arg Ser Ser Thr Cys
260 265 270
Gly Ala Gly Thr Pro Pro Ala Ser Ser Cys Pro Ser Leu Gly Arg
275 280 285
Gly Trp Arg Pro Leu Pro Ala Ser Leu Pro
290 295

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<210> 132

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2899137

<400> 132

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Met Ala Ala Ser Met Ala Arg Gly Gly Val Ser Ala Arg Val Leu
1 5 10 15
Leu Gln Ala Ala Arg Gly Thr Trp Trp Asn Arg Pro Gly Gly Thr
20 25 30
Ser Gly Ser Gly Glu Gly Val Ala Leu Gly Thr Thr Arg Lys Phe
35 40 45
Gln Ala Thr Gly Ser Arg Pro Ala Gly Glu Glu Asp Ala Gly Gly
50 55 60
Pro Glu Arg Pro Gly Asp Val Val Asn Val Val Phe Val Asp Arg
65 70 75
Ser Gly Gln Arg Ile Pro Val Ser Gly Arg Val Gly Asp Asn Val
80 85 90
Leu His Leu Ala Gln Arg His Gly Val Asp Leu Glu Gly Ala Cys
95 100 105
Glu Ala Ser Leu Ala Cys Ser Thr Cys His Val Tyr Val Ser Glu
110 115 120
Asp His Leu Asp Leu Leu Pro Pro Pro Glu Glu Arg Glu Asp Asp
125 130 135
Met Leu Asp Met Ala Pro Leu Leu Gln Glu Asn Ser Arg Leu Gly

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	140		145		150
Cys Gln Ile Val	Leu Thr Pro Glu Leu	Glu Gly Ala Glu Phe	Thr		
	155		160		165
Leu Pro Lys Ile	Thr Arg Asn Phe Tyr	Val Asp Gly His Val	Pro		
	170		175		180
Lys Pro His					

<210> 133
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2986229

<400> 133

Met Trp Arg Lys Pro Asp Val Leu Tyr Ser Val Ile Pro Val Thr		
1	5	10
Ser Leu Phe Phe Leu Leu Ala Leu Asn Leu Pro Asp Val Phe Gly		15
	20	25
Leu Val Val Leu Pro Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu		30
	35	40
Leu Asp Val Arg Ser Val Leu Ser Leu Ser Ala Val Cys Arg Asp		45
	50	55
Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp Arg Phe Leu Tyr		60
	65	70
Leu Arg Asp Phe Arg Gly Asp Phe Arg Asn Asp Ile Phe Thr Arg		75
	80	85
Lys Gly Ser Tyr Cys Leu Asp Tyr Ser Ala His Gln Lys Phe Leu		90
	95	100
Val Val Gly Phe Phe Cys Cys Lys		105
	110	

<210> 134
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 3222081

<400> 134

Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val		
1	5	10
Leu Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro		15
	20	25
Arg Ile Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg		30
	35	40
Thr Ile Arg Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu		45

	50		55		60									
Val	Val	Ser	Glu	Ser	Cys	Val	Glu	Val	Gln	Glu	Ile	Asn	Glu	Glu
	65		70		75									
Glu	Tyr	Leu	Val	Ile	Ile	Arg	Phe	Thr	Pro	Thr	Val	Pro	His	Cys
	80		85		90									
Ser	Leu	Ala	Thr	Leu	Ile	Gly	Leu	Cys	Leu	Arg	Val	Lys	Leu	Gln
	95		100		105									
Arg	Cys	Leu	Pro	Phe	Lys	His	Lys	Leu	Glu	Ile	Tyr	Ile	Ser	Glu
	110		115		120									
Gly	Thr	His	Ser	Thr	Glu	Glu	Asp	Ile	Asn	Lys	Gln	Ile	Asn	Asp
	125		130		135									
Lys	Glu	Arg	Val	Ala	Ala	Ala	Met	Glu	Asn	Pro	Asn	Leu	Arg	Glu
	140		145		150									
Ile	Val	Glu	Gln	Cys	Val	Leu	Glu	Pro	Asp					
	155		160											

<210> 135

<211> 865

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 443531

<400> 135

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attcctcaat tttccagtct cccttgagct aagtgtggcc ctatgactca cttccagcca 60
tgaaaacaag tgcaaatctg ttaggagtat gttctggggc aatTTTTgct ctctgatga 120
agacaaaggc tgttgatcca ctgaaccac ccagacacta tgtggtttct tgaatgtcct 180
acgtacattt tgatggatta cccaaggact atctgatgaa gaataataga gacatatataa 240
tacatatggg ctacatcttg gcaaaataaa gtaatcctga agtaaattct aaggatgttc 300
tgaattgaca cctcttaagc acaaccgaat gtctggtgg ctttgctcc cactggggct 360
ttttggctct tgtttggccc cagcggctgc tgcagctctg tctgaattca cacaggagca 420
acatgatggg gctcagccct cgccgaagtg tcttgctgaa gagttgggag atgcttggac 480
tattcagata gaagccaact ggaagtacag ggcagtcaac acaaaccaga gaggcaaact 540
tttggccagt gagacatgga aagggagaag aaatacatte ttctttctcc cctagagtga 600
ggaccaacct gagtcccgat cacctggaat cccctcagac gagcgtccct tgagatccag 660
cacatggcag ccagcgtgct gacgattcct tcctgcctac tggctccttc ttatttctgc 720
ctccgtggaa ctgtattctc taatcaatat tagcacatac atattgcccc agactgtacc 780
tcctgggaac ccaggataaa gcactatcta aacattttgt cttggaattg taataaactt 840
caaaagaaaa atacaaaaaa aaaaa

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865

<210> 136

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 11, 12

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 632860

<400> 136

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ttgctggctc agcctgctct ttgctccttc atgggacccc agtggatcct gcagttctgc 180
tcttggtctg aaccacgcca gcttcgctgg agctggactg agccgccttt tacattattg 240
gactctctcg gggtgagagc tgcccaggac tctgcagtt tcaccaccct tgttcctttg 300
actcttgact catcattcat gaccgttaac gtggttccat ttgtatggac ttcttctttc 360
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cagaatgtgt cctggaagcc aggcaccttc tggggtgtat ttggggcgct caacaaggct 540
tgatcgagct ttgggggtag atctagctat tccatgggga ttcttttcag aattgctgtt 600
ttcggttaact aattccatga ccaggtccat ggcattggat gacattgcgc tacactgttg 660
ctcaccgggg tcaccctgcc tcacagggtg gatggcaagc atgttg 706
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<210> 137

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 670010

<400> 137

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cccgggagca cctcccctcc cgaggcagtc tgctcagagg gcctcgcccc agaattccag 180
ttctggtttc atgccagcct gtaaaaggcc atggaacttt ggggtgaatca ccgatgccat 240
ttaagagggt tttctgccag gatggaaatg ttaggtcggt ctgtgtctgc gctgttcatt 300
tcagtagcca ccagccacct gtggccgttg agtgcttgaa atgaggaact gagaaaatta 360
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ggggtacatg tgatatttgg atacatgtat acaatatata atgatcaaat cagggttaact 480
gggatatcca tcacatcaaa catttatatt ttattctttt tagacagagt ctactctgt 540
caccagggt ggagtgcagt ggtgccatct cagcttactg caacctctgc ctgccagggt 600
caagcgattc tcatgcctcc acctcccaag tagctgggac tacaggcatg caccacaatg 660
cccaactaat ttttgatatt ttagtagaga cgggggtttg ccatgttgcc caggctggcc 720
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gcgtgagcca ccgtgcctgg g 801
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<210> 138

<211> 664

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 505, 518, 527, 540, 565, 566

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 726498

<400> 138

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gcagagccat gatgagtctt acggaaataa gggttaaaaca tatgcttgaa atttggcatg 180
gcagacaagc cagagcttgt gaaaatctaa gaaaccaaac acgtgtagcc accaaagtgg 240
aaccacaaaa gggaagatct acagaaatct gttgccttgc tgtagttcca ttaaagtagg 300
ttgtgcagtc aagcatcttg tgggtgggtct ggagctgttg ccagcatcag gaagacaagc 360
tgggtgctaa gtgaagaaat acacaatgta gaaactgtca ggcattctct cccctggact 420
tcaccatatt tgatgatgtt ctcagagtca gggcactgct tcacttttct cttccaaatc 480
tcacacaaaa ttctctgtta ggcancccca gcttagancc ttacaantga gggggatcan 540
ggaaatggag taccagata cccanngtga tatactttta tgcctcagc ttcttatctt 600
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acta

```

664

<210> 139

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 795064

<400> 139

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taaagtttca gaagagactt gtgcacataa gggcttcctc tcaagtgtat tgcagtaatg 120
gctgaatcgg gggttaacatc ccttccaggc acagcgagtt gggtctgctt ttgcttgta 180
agccaaagaa aagccacatc taaaaagcta ctactaaaag ccagaaagaa aagtggattt 240
gaactcagtg tcacagactc ttctgagtgt tttagggcca cagctagtgt aagaggcatg 300
aagaatagac atgcaaaaagg gaacgggtgc accagagacc cctgttttgg ctgacagacc 360
atatgtccca ccagctgggg aatctgacaa gaggacatag gtggcactct ttttttaaag 420
ctatttattg tatctatttt taaataaaat tgccatcctt cattcagctc ttagaacaaa 480
agcaaaaaac cctgtaaatc aggagatata agcacatctg caccagaat agggccatat 540
gatagggcaa cctgagctt aaacaatgac atcttcaagg gtagaactaa tctgaaaccc 600
ccttccagcc tctggaagac actggcctgc atcagttaga gtcagagcaa gtgtcacttc 660
acagggaaaa gaaggattat atagacttcc tatccctaga gttataaat gtcaactata 720
taaaaaaagc tcaaaacagt gttaaaggaa tgaacagtag aattttaata ggctgtccaa 780
agaagccagg tctgctgtgg gcaagtatag cctaacccta gtcttgtaaa ataagccaga 840
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tatcacttga gaacctctc agcaaatgag ccagaaaaca ttcaatcaag ttggcaaatg 1020
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cagcactgtc ctggagctaa tacactgttt cactgcctct gccatataat gatgccagca 1140
ctagccagct ggtgggtatt tggaggaatc ctgcatgagg attgcccaat aaggggcagg 1200
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1241

<210> 140

<211> 750

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 570, 641

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 924925

<400> 140

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cctctcaggt gccctactt gctttctgct tccttctggt gaagtcacc tccaacatta 180
acctgcccac cccacccccg tcatccctgg agaattccag ctttgtcgta tctcagagag 240
ggaatctaata tgtttttggg gggcaaaaga aagcaacgtt taggtatcac tctacttgg 300
accgcatgcc tttttatagc caaatttctg tgtatttcgt aaatggattt cgcgttaatg 360
gatatttatg taataactag acttctcaga ttattgtgag aagggtcagg ttggaagggg 420
tgtaggaaga cgggtgaggg gtagtttttt tctgtcctag tttttttttt ttttattgtc 480
atctctgagg tggactttgt cacctgtggt tattggggcc aagtggactc agctccgggg 540
gagaaggctt ctctgccatt tcggtccaan ggtgactgac acaggcgtac tttttgggac 600
tgtggaagca tcagatgcca gcactgactt cagaccagca ntctgggcta gaggaagatg 660
ggacctttca ggatggaaat accttggact ttcttttggg cctcgggaaa ctggggcttt 720
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<210> 141

<211> 1235

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 962390

<400> 141

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atgggggtcac tcaacaaaaa cacctctcag cctccatggg tggctctgtg gaaatccccct 240
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ggggccactt ccacgggcag tccttctaca gcacaaggcc gccttccatt cacaaggatt 360
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caaacctgcy gaaggaggac cagtctgtgt atttctgccc agtcgagctg gacaccggga 480
gatcaggagg gcagcagttg cagtccatca aggggaccaa actcaccatc acccaggctg 540
tcacaaccac caccacctgg aggcccagca gcacaaccac catagccggc ctcagggtca 600
cagaaagcaa agggcactca gaatcatggc acctaatgtt ggacactgcc atcagggttg 660
cattggctgt cgctgtgtct aaaactgtca ttttgggact gctgtgctc ctcctcctgt 720
ggtggaggag aaggaaaggt agcagggcgc caagcagtga cttctgacca acagagtgtg 780
gggagaaggg atgtgtatta gcccggagg acgtgatgtg agaccgctt gtgagtcctc 840
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tagcgtgaaa tgctgtgac acttaaaaaa aaaaa 1235
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<210> 142

<211> 1834

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1259405

<400> 142

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ctgggcccccc agcgatggcg accctgtggg gaggccttct tcggcttggc tccttgctca 180
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tttataataa gaacatatct cagaaagatt gtgattgcct tcatgttgtg gagcccatgc 360
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gaagctctgt cacaatcaag gttaccatta taatttatct ctccattttg ggccttctac 480
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ttgaaacatc catcagtgtg tctatctatg tctcctagtt ttttctctct ccctcttttg 1800
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1834

<210> 143

<211> 1722

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1297384

<400> 143

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ctcgctcccc cacctccttg ggtcatgccc acccaccctt tectgcctcc tccgtgtgaa 180
gacatccaac atccacgtga cttttccagc tccattttta aacagtgact gagattctag 240
aaaaactggc tgctaactgg cctgagccag gcaacactga ttccaatccc tectcctttt 300
ttaagttatt tgatggaaga ctcacctaat ttgtgacctg aaactgttga agaaatagag 360
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ctaggttact ggggttgagg ggattgtttt cttttggggg ccttccccct ttactccttt 480
tcttccagag atcaagagct tctcttgcac cttcttccac tgggctctgg attaataaat 540

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```

taccctaaagg ctgcacctgc cgtgttgtct gggcttgcac cccagatgtg ttggagtatg 600
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cattttatag ccaaggacgc ctcgctaaag tcttatgggc gtcccctggg gttggggggg 720
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ggatagtgtt aaataaactt ctctgttctc taaaaaaaaa aa 1722

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<210> 144

<211> 1741

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1299627

<400> 144

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tgtggcaaaag attgcaaatc ttactgctgt gatggaacca cgccctactg ttgctcctac 180
tacgcttata ttgggaatat cctctcgggc actgcaattg cgggcattgt ttttggaaata 240
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cacaggcgga cccgcgtggg catcctcagg acgactcaca tcaacaccgt ctctcctat 360
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ccatactccc ccaccccaca ggggtccagca cagcgttctc caccctctcc ttatcctgga 480
aacgcaagga aataatctat ctcccagaac agaacatgtg ccaatgggag atcttgctgt 540
gaataaaatg cctctactca gaaacaggca ggaaagaatt gctccaagga atactttttg 600
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tcaagttcca caggtagcag acacttcact tccaagtaaa agatgagaaa tcaattatct 1440
ccacaggatt ttaggtcagg gagcaaaaat ctcagaactt gaccatgaag atacacaaca 1500

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gactcgcaaa aataaagtgg gaaatgaagt tcagattccc ttctgtagat ttccttaaaa 1560
ctattatttt ttcttcttc gtaaaatttt gataatctgt tctcttaaaa aagttaatga 1620
cacaattaag atactgacat caaattgttg ccttttacca aaatgcaa atttatgaagt 1680
gcctaccttt atatgtataa agcattta ataaattct aatgtgccat aaaaaaaaaa 1740
a
1741

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<210> 145

<211> 997

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 973

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 1306026

<400> 145

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tgctacggac gacgcctatg aagcccttag tccttctagt tgcgcttttg ctatggcctt 180
cgtctgtgcc ggcttatccg agcataactg tgacacctga tgaagagcaa aacttgaatc 240
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aaactgaggc accaagaatg ttgccagtgt ttactgaatc atctacaagt ccatatgtta 660
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aatcagaaga tgttcctcag ctctcagggtg aaactgcgat agaaaaaacc gagagtggga 780
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tcgaatcatg tcatagctgt ttctgtgtg aattggtatc gctcacaatg cacacacata 960
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997

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<210> 146

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1316219

<400> 146

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tcaagtaatt ccttgtctgg aattttctgt tgatctcatg ggtactaaga aacgaaatat 120
tctgttcatt ttcattttta aagaatatcg ataacttgat gacccagaa ggagttggcc 180
ttaccactgc cttacgtgtt ctctgtaatg ttgcatgccc accacctcct gttgaaggtc 240
aacagaaaga tctgaaatgg aatcttgccg ttattcagct tttttctgct gaaggaatgg 300
acacgtttat tcgagttctg caaaaattga acagtattct gactcagcct tggaggctcc 360

```



```

atgtcaacat ggggactacc cttcacagag ttactactat ttcaatggct cgctgcacac 420
tcactcttct taaaactatg ttaacggaac tcctgagagg tggatccttt gaggtttaagg 480
acatgcgtgt tccttcagcg cttgttactt tacatatgct cctgtgctct atccccctct 540
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<210> 147

<211> 526

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte Clone No: 1329031

<400> 147

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gtttagaagc gctcatctgg cttttcgctt gcttctgcag caactccac gactgttgta 480
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<210> 148

<211> 2090

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1483050

<400> 148

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gcttagcctc atttccacca tctacatggc agcctccatt ggcacagact tctgggtatga 240
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<210> 149

<211> 2403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1514160

<400> 149

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<210> 150

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1603403

<400> 150

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tgactttgca actgaagctg aaggagtctt ttctgacaaa ttctcctat gaggccagct 180
tcttgggaatt gcttgaagag ctctgcctcc tctccatct ccttcaggg accagcgtca 240
ccctccacca tgcaagatct caacaccatg ttgtctgcaa cacatgacag ccattgaagc 300
ctgtgtcctt cttggcccg gcttttgggc cggggatgca ggaggcaggc cccgacctg 360
tctttcagca ggccccacc ctcttgagt gcaataaata aaattcggtg tgctgaattc 420
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<210> 151

<211> 2109

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1652303

<400> 151

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gcttcagttc agatttcaag ctgtgttggt gttgggacca gcagaaggca aacgtccagc 240
caacacacag gactgtaaga ggactctgag ctacgtgcc tgtgaagacc cccaggcttt 300
gtcataggag gtcgttcagc ttcccaaag tcagaggtga tttgatttgg ggaagactga 360
atattcacac ctaagtcgtg agcatatct gagttttact tccttatggc ttgccctcca 420
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agttctctct ctcatacaca cacacaccct tgctccagaa tcaccagaca cctccatggc 480
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aaaaaaaaa 2109

<210> 152

<211> 1114

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1693358

<400> 152

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<210> 153

<211> 2192

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1707711

<400> 153

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<210> 154

<211> 913

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1738735

<400> 154

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<210> 155

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1749147

<400> 155

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aaagggtacct ggtaagaatg tttgaaagat cttccatttc taggaacccc agtcctgctt 420
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<210> 156

<211> 545

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1817722

<400> 156

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ctgttacaag ctgcttcagc tttagctaat tacattcatt tctccagtta ctccaaagat 120
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ggaatagggg taccatttat gggaagtttg gcagaatttt ttgacatcgc ttcccaaatt 180
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<210> 157

<211> 1746

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1831290

<400> 157

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gaagcctaca tagaccccat tgccatggag tattacaact gggggcggtt ctcgaagccc 480
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<210> 158

<211> 2011

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1831477

<400> 158

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<210> 159

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 440

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 1841607

<400> 159

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atccccccct ctgctgggcg tggtgactca tgtctataat cccagctctt tgggaggcca 240
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<210> 160

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1852391

<400> 160

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cttttgttta gagttaatgc tccttttatg tcaccagttg ctttgctttt taaattattt 480
caaattggca ctttgggggc tgcctaagaa ttgataagcg gggatgatc tgttgatgaa 540
tc
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542

<210> 161

<211> 1066

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1854555

<400> 161

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ggcactgtgc tcggagtcgg tgcgggcgtg ttcattcttag ccctgctctg ggtggcagtg 180
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<210> 162

<211> 1173

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1855755

<400> 162

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gccgagctcc cggggccctt tctctgcggg gccctgctag gcttctctgt cctgagtggg 180
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caagtcaaca acccaccaga tttctacacc aatgggttgg ggctaataca cttactgtg 540
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<210> 163

<211> 890

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1861434

<400> 163

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tccaaactgg cgaatttgct gatcttcgct tcctctccg ctttccggcc ggcagcgtg 180
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atgtccttgg ctgagagagt actactcacc tggcttttca cactactctt cttgatcatg 300
ttggtgttga aactggatga gaaagcacct tggaaactgg tctcatatt cattccagtc 360
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gaatcacgga cttctagtca acctacagct taattattca gcatttgagt tattgagatc 840
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<210> 164

<211> 806

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1872334

<400> 164

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<210> 165

<211> 1923

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1877230

<400> 165

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catagaatca acatatggta gggattacag tgggggcatt tctttatatc acctcttaaa 1860
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aaa

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1923

<210> 166

<211> 518

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1877885

<400> 166

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atctgggttc catcctcttc ctgcttttgc tcccagtggc tgcagctcag acgactccag 180
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gcaaagtcta catcaacatg ccaggcaggg gctgaccctc ctgcagcttg gacctttgac 420
ttctgaccct ctcatcctgg atggtgtgtg gtggcacagg aacccccgcc ccaacttttg 480
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518

<210> 167

<211> 1631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1889269

<400> 167

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agtgaaggag tgcagaggca tcacctgaaa gtttacaagt ccttccactt tctctctgag 420
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<210> 168

<211> 1548

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1890243

<400> 168

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<210> 169
<211> 616
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1900433

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<210> 170
<211> 1981
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1909441

<400> 170
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<210> 171

<211> 1492

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1932226

<400> 171

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<211> 1613

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1932647

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<210> 173
<211> 1622
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2124245

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<210> 174

<211> 1320

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2132626

<400> 174

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<211> 778

<212> DNA

<213> Homo sapiens

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<223> Incyte Clone No: 2280639

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<211> 1477

<212> DNA

<213> Homo sapiens

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ttttccccga gggcttccat gccagcttgc cttccccccg cctgaagctc cgcagacttg 1140
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tgtcggcgcc cagggggaat attaatagct cccggggggg ggggaatact ttgaaggcag 1260
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cggcttcaag caatttcgca gagcaagatt tgcgggcgcc ggaaccata aagtggtgaa 1440
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<210> 177
<211> 682
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2349310

<400> 177
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cgttgtcttc ttctcttcac caccacccag gagctcagag atctaagctg ctttccatct 180
tttctcccag ccccaggaca ctgactctgt acaggatggg gccgtcctct tgccctcttc 240
tcatectaata ccccttctc cagctgatca acctggggag tactcagtgt tccttagact 300
ccgttatgga taagaagatc aaggatgttc tcaacagtct agagtacagt cccctctcta 360
taagcaagaa gctctcgtgt gctagtgtca aaagccaagg cagaccgtcc tcctgccctg 420
ctgggatggc tgtcactggc tgtgcttggt gctatggctg tggttcgtgg gatgttcagc 480
tggaaccac ctgccactgc cagtgcagtg tgggtggactg gaccactgcc cgtgctgcc 540
acctgacctg acagggagga ggctgagaac tcagttttgt gaccatgaca gtaatgaaac 600
caggggtcca accaagaaat ctaactcaaa cgtcccactt catttggtcc attcctgatt 660
cttgggtaat aaagacaaac tt 682

<210> 178
<211> 1508
<212> DNA
<213> Homo sapiens

<220>
<221>
<222> 11, 139
<223> a or g or c or t, unknown, or other

<220>
<221> misc_feature
<223> Incyte Clone No: 2373227

<400> 178
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atacgcaaac cgcttctcnc cgcgcggttg ccgattcatt aatcagcttg caccgacagg 180
ttcccgaactg gaaagcgggc agtgagcgca acgcaattaa tgtgagttag ctactcccc 240
accccccttc ccgcgggcct cgggttcaaac gaccgggtgg gtctacagcg gaagggaggg 300
agcgaaggta ggaggcaggg cttgcctcac tggccaccct cccaacccca agagcccagc 360
cccatggtcc ccgcccgcgg cgcgctgctg tgggtcctgc tgctgaatct ggggtccccg 420
gcggcggggg cccaaggcct gaccagact ccgaccgaaa tgcagcgggt cagtttacgc 480
tttgggggcc ccatgaccgc cagctaccgg agcaccgccc ggactgggtc tccccggaag 540
acaaggataa tcctagagga cgagaatgat gccatggccg acgcccagcg cctggctgga 600
ccagcggctg ccgagctctt ggccgccacg gtgtccaccg gctttagccg gtcgtccgcc 660
attaacgagg aggatgggtc ttcagaagag ggggttggtg ttaatgccgg aaaggatagc 720
accagcagag agcttcccag tgcgactccc aatacagcgg ggagttccag caccgaggtt 780
atagccaata gtcaggagcc tgaaatcagg ctgacttcaa gcctgccgcg ctcccccg 840
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```

cggagccggt ctgggaagct gcaaggcctt tccgggcgcc ttcgagttgg ggcgctgagc 1080
cagctccgca cggagcacia gccttgcacc tatcaacaat gtccctgcaa ccgacttcgg 1140
gaagagtgcc ccctggacac aagtctctgt actgacacca actgtgcctc tcagagcacc 1200
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gaggatattt ggaatagcct ctcttcagtg ttcacagaga tgcaaccaat agacagaaac 1380
cagaggtaat ggccacttca tccacatgag gagatgtcag tatctcaacc tctcttgccc 1440
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aaaaaaaaa
1508

```

<210> 179
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2457682

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<400> 179
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gagcagaact gctctggggg cgctctgaat cacttccgct cccgccagcc aatctacatg 180
agtctagcag gctggacctg tcgggaacgac tgtaagtatg agtgatatgt ggtcaccgtt 240
gggctctacc tccaggaagg tcacaaagtg cctcagttcc atggcaagtg gcccttctcc 300
cggttcctgt tctttcaaga gccggcatcg gccgtggcct cgttttctcaa tggcctggcc 360
agcctgggtga tgctctgccc ctaccgcacc ttcgtgccag cctcctcccc catgtaccac 420
acctgtgtgg ccttcgcctg gctttctgga agatgacagc ctgtagctgc tgaaggaatc 480
agaggacaag ttcaggctgg actgaagacc cttggagcga gtcttcccc gttgggggata 540
ctgccccgcg cctgctgg
558

```

<210> 180
 <211> 502
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2480426

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<400> 180
cttggagtct gggaggagga aagcggagcc ggcagggagc gaaccaggac tggggtgacg 60
gcagggcagg gggcgccctg ccggggagaa gcgcgggggc tggagcacca ccaactggag 120
ggtccggagt agcgagcgcc ccgaaggagg ccatcgggga gccgggaggg gggactgcga 180
gaggaccccg gcgtccgggc tcccggtgcc agcgctatga ggccactcct cgtcctgctg 240
ctcctggggc tggcgggcgg ctgcctccca ctggacgaca acaagatccc cagcctctgc 300
ccgggactgc cgggacctcg aggggacccc gggccgcgag gagaggcggg acccgcgggg 360
cccaccgggc tagccgggga gtgctcggtg cctccgcgat ccgccttcag cgccaagcgc 420
tccgagatcc ggggtgcctcc gctgtctgac gcacccttgc cttegaccgc gtgctgggtga 480
acgagcaagg acattacgac gc
502

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<210> 181
 <211> 1659
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2503743

<400> 181

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agggattcca gggctcctct tccttctctt ctttctgctc tgtgctgttg ggcaagtgg 180
cccttacagt gccccctgga aaccacttg gcctgcatac cgctccctg tcgtcttgcc 240
ccagtctacc ctcaatttag ccaagccaga ctttgagacc gaagccaaat tagaagtatc 300
ttcttcatgt ggaccccagt gtcataaggg aactccactg cccacttacg aagaggccaa 360
gcaatatctg tcttatgaaa cgctctatgc caatggcagc cgcacagaga cgcaggtggg 420
catctacatc ctacagcagta gtggagatgg ggcccaacac cgagactcag ggtcttcagg 480
aaagtctcga aggaagcggc agatttatgg ctatgacagc aggttcagca tttttgggaa 540
ggacttcctg ctcaactacc ctttctcaac atcagtgaag ttatccacgg gctgcaccgg 600
caccctgggt gcagagaagc atgtcctcac agctgccac tgcatcacg atggaaaaac 660
ctatgtgaaa ggaaccaga agcttcgagt gggcttecta aagcccaagt ttaaagatgg 720
tggtcgaggg gccaacgact ccacttcagc catgcccagc cagatgaaat ttcagtggat 780
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gaggatgtgg aagagacagc agcagaagtg ggagcgaaaa attattggca ttttttcagg 1140
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taaggtgtct tataatcttt tacctatttc ttacaattgc aagatgactg gctttactat 1440
ttgaaaactg gtttgtgtat catatcatat atcatttaag cagtttgaag gcatactttt 1500
gcatagaaat aaaaaaaaata ctgatttggg gcaatgagga atatttgaca attaaagttaa 1560
ctttcacgtt tttgcaaact ttgattttta tttcatctga acttgtttca aagatttata 1620
ttaaatattt ggcatacaag agatatgaaa aaaaaaaaaa 1659
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<210> 182

<211> 2015

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2537684

<400> 182

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cccagcactc ggtgtggaaa ggcccctacc tgctgtaaga ttatgggtcc atgaaagcag 120
taagctggac acagaggtgt agtgtgcggg acagagggcc ttgcagatgc ctttctgttg 180
gtgttttagt gttaaaaatac ggagagtatg gaactcttca cctccatttt ctcagcggct 240
gtgaagcagc ctccatgctt cggaagtacg gacactacgt cgcgttttca agcgtgtctg 300
ttctgcaggt aacagcatca agctgcacgt ggaagcatct cgcggttttc tagaaacagg 360
cattttctta tccctctccc gctccttttt ccacaaaggt gaatttcata aatgtaatac 420
tagtaaaagt aatgaattac tgagtttata cagaaattta ggtaacttct cctttagtct 480
caagagcgag tcttgctttt taatgggtgc cgtttatgtt gctgccgccc ctgtgtgcct 540
ggctcctctg ggtgccttgg tgtctgctgg tggctggcag tgggcgcagc ggaggagagt 600
```

```

tgtgctgcag ctcatacggg gtgtctgtca tctcagtcgt gagtaaatgc agtgtctgcc 660
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cgctgcctgg cagccaaggg tgttggtcgc gaagctggga gtggcctctg gtggagcctg 780
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aatgacaccg tgattgagct tgtcagcaga gctgaaagag aaagtagaag gatgtgcatt 900
gtttcttcta agatatcttg catgtatctg tgtattcaaa ttcaaacaga gatgggttgt 960
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gtatttttag tagagatggg gtttcaccat gtctcaaaact cctgacctca ggcgatccac 1920
ccacctcagc gtcccaaagt gctggggata taggggtgac caccgcacc tgcgccaaga 1980
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```

2015

<210> 183

<211> 740

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2593853

<400> 183

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ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc ttggagtctt 60
tctagctcct gccctagcta actataatat caacgtcaat gatgacaaca acaatgctgg 120
aagtgggcag cagtcagtga gtgtcaacaa tgaacacaat gtggccaatg ttgacaataa 180
caacggatgg gactcctgga attccatctg ggattatgga aatggctttg ctgcaaccag 240
actctttcaa aagaagacat gcattgtgca caaaatgaac aaggaagtca tgccctccat 300
tcaatccctt gatgactgg tcaaggaaaa gaagcttcag ggtaaggagc caggaggacc 360
acctcccaag ggctgatgt actcagtcaa cccaaacaaa gtcgatgacc tgagcaagtt 420
cggaaaaaac attgcaacaa tgtgtcgtgg gattccaaca tacatggctg aggagatgca 480
agaggcaagc ctgttttttt actcaggaac gtgctacacg accagtgtac tatggattgt 540
ggacatttcc ttctgtggag acacgggtgga gaactaaaca atttttttaa gccactatgg 600
athtagtcat ctgaatatgc tgtgcagaaa aaatatgggc tccagtgggt tttaccatgt 660
cattctgaaa tttttctcta ctagttagt ttgatttctt taagtttcaa taaaatcatt 720
tagcattgaa aaaaaaaaaa

```

740

<210> 184

<211> 748

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2622354

<400> 184

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tgcattctca ggctcctctg ctcacacgga gcccagtgag ccccatgac tccttacctg 120
atgctgtgcc agccacacaa gagatgtggg gacaagttct acgacccctt gcagcactgt 180
tgctatgatg atgccgtcgt gcccttggcc aggaccaga cgtgtggaaa ctgcaccttc 240
agagtctgct ttgagcagtg ctgcccctgg accttcattg tgaagctgat aaaccagaac 300
tgcgactcag cccggacctc ggatgacagg ctttgtcgca gtgtcagcta atggaacatc 360
aggggaacga tgactcctgg attctccttc ctgggtgggc ctggagaaag aggctggtgt 420
tacctgagat ctgggatgct gagtggctgt ttgggggcca gagaaacaca cactcaactg 480
ccactttcat tctgtgacct gtctgaggcc caccctgcag ctgccctgag gaggccca 540
ggcccccttc tagaattctg gacagcatga gatgcgtgtg ctgatggggg cccaggggact 600
ctgaaccctc ctgatgacct ctatggccaa catcaaccgg gcaccacccc aaggctggct 660
gggaaccctt cacccttctg tgagattttc catcatctca agttctcttc tatccaggag 720
caaagcacag gatcataata aatttatg 748
```

<210> 185

<211> 648

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2641377

<400> 185

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ggctcagatt ctttccccgc tgtctgtggg tccacactcc cagtggcacc tccaggagag 120
aatctgattg gctcagttcg ccagataact caactttccc attggctacc tttgggtcag 180
gtgatctcca ctgacctat cgctatgcc tgatggtggg tcacatggtg caaatgttgc 240
ctgagagctt agtggattag ggatgtggct gggctcatgg ttgacgtccc tgctgctgag 300
cccttacggg tcaggctggg agaaggtacc atgttgtgtg actggtcatt tgaggctctg 360
cagctgttgc ttgctgggct tggcagggtg tcaaagtgc catttttctg aagggttttt 420
ttctgagtat tcctcagatg tactccccctg gggccgacgg tctttccttc cacagggcga 480
tgcttcctca cttgcttgtg aatgtttcct tcattctccag gttgtctggg gacaattctg 540
tcttttgagg gcctgggcag gatttacaga gggctccatg ccagctcctt cctgccgggt 600
ccacttctgg tgtagggtaa acacctgcgc attcatgtcc tagtggtg 648
```

<210> 186

<211> 2110

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 1932

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 2674857

<400> 186

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ctgcttcctg ccgaggctgg cccaggcagc cgcgcttcga aggacgccgc cgggagctgc 180
ggacatgcgt ggagtggcag tgctaacggc tgggtgtctcg cactgttggc ctgtgaaggt 240
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cagtacgacc atcttgagtt ccccggagtc gtccccagga cgttccctcg gccaagtgtg 480
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tactctcagc taatagttag aggagtgcct gccatcggcg tgatttttgg actctggacg 600
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<210> 187

<211> 773

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2758485

<400> 187.

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cctctgcctg gccgcggctc tgggaagtgc gcagtcgggg tcgtgtaggg ataaaaagaa 180
ctgtaaggtg gtcttttccc agcaggaact gaggaagcgg ctaacacccc tgcagtacca 240
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tcctggaata tataaatgtg ttgtttgtgg aactccattg ttaaagtcag aaaccaaatt 360
tgactccggt tcaggttggc cttcattcca cgatgtgac aattctgagg caatcacatt 420
cacagatgac ttttccctatg ggatgcacag ggtggaacaa agctgctctc agtgtggtgc 480
tcaccttggg cacatttttg atgatgggcc tcgtccaact gggaaaagat actgcataaa 540

```



```
ttcggtctgcc ttgtctttta cacctgcgga tagcagtggc accgccgagg gaggcagtgg 600
ggtcgccagc cgggccagg cagacaaagc ggactctgag agtaatggag agtgatggaa 660
acaaagtgtta cttaatgcac agcttattaa aaagatcaaa attgttatcc taatagatat 720
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<211> 714

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<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2763296

<400> 188

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<210> 189

<211> 609

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<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2779436

<400> 189

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<210> 190

<211> 1088

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2808528

<400> 190

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<210> 191

<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2809230

<400> 191

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<211> 985
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2816821

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<213> Homo sapiens

<220>
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<223> Incyte Clone No: 2817268

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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Incyte Clone No: 2923165

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<220>
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agtggatttc cttctatggt tgtcagtga attgcgctat aattcgcgtt gctgtcctca 600
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<210> 196

<211> 893

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2992192

<400> 196

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<210> 197

<211> 1730

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2992458

<400> 197

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<211> 2029

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte Clone No: 3044710

<400> 198

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<220>
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<220>
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<210> 201
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 674760

<400> 201

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<210> 202

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1229438

<400> 202

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<210> 203

<211> 936

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1236935


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<210> 204

<211> 432

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1359283

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<210> 205

<211> 971

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1450703

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tgcccatgag atcaaccatg gtattggaca agcaggaaag gaagcagaga agcttggcca 420
tggggccaac aacgctgctg gacaggccgg gaaggaagca gacaaagcgg tccaagggtt 480

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971

<210> 206

<211> 1832

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1910668

<400> 206

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1832

<210> 207

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1955143

<400> 207

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<210> 208

<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1961637

<400> 208

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<210> 209

<211> 1355

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1990762

<400> 209

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<210> 210

<211> 776

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1994131

<400> 210

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<210> 211

<211> 817

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1997745

<400> 211

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<210> 212

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2009035

<400> 212

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acagacataa agcataaaaa ccgagatata tatttgatca tataaaaaat taagctgggc 360
acagtggctc ataccctgta tcccagcact ttggggaggcc aagggtgggg tagactgggt 420
gagctcaggg gttcaagacc agcctgggaa catggtgaaa cccaactcta ccaaaaaaaa 480
aaaa 484
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<210> 213

<211> 509

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2009152

<400> 213

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cccagtttat taccattaga ccataccttt ttgtccaatc atttaaaaca aattttttata 60
taataagttt tatttgtatg taataaattt tattatataa aaataagttt taatatatat 120
```

```

tatataaaaa gttttaataa atacctaata tattatttta tatgataaaa cttatatataa 180
atgaaatttt atgctgttct cttgtcaatc tgtcttttgt tatcttgctg gtgtgcctgt 240
catgtgaggg actgcaatct gatatgccta tttccacag tcaaagcaat tacaagagaa 300
ttgttacaat taccaggtta tgtcaagaga ttttttttta attcactaag gtagagataa 360
ggagaatgta ttaaaatagg atatttttaata tataaatgca tgactgggga ggggggtattg 420
tttttgaata aaatatgagg ttatttgcca tgacaaaaaa aaaaagaagt aggaaaatcc 480
catggaaatt tatgttcctt ctaactttt

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509

<210> 214

<211> 1130

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2061752

<400> 214

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ggatttatca cattctgcct tgaatcatag ggaacagcat gtgtagtgga atgaacacag 60
gcctctgaat ccaagatatg agtttaaate ccagcttttg aggtgggttac ttaaagtctc 120
agtgccttca ttcttcttcc tatataaagt agatattaca atatctaact tacagagtca 180
ttgggagcta tacatgcagc gattgggttaa agcacctggc acatggcaag cgattagcaa 240
atgctgggta cttctacttc tttctcttcc cttttcccag tctatcataa tttccttgag 300
agcaggcacc atgtcttatt tacccttgta tttcccacag tacttcccat agtgagttac 360
ccttagtaaa tactcagtaa gttgaattga atttaaatta cctgtaagtc ttaaaatgtg 420
ggattaaatt aagaatatat tgccttgga ataccctaat gtctattgat ggatgaatgg 480
ataaacaaaa tgtggtatac acataatgga atattattca gccttaaaaa ggaatgaaat 540
tctgacatgt gctacaatat gatgaacctg gaagacatta tatgtgaaat aagccagaca 600
gaaaaggaca aatactatat gattccactt atatgaagta cctagagtag tgtaattcat 660
agaaacagaa agtacagggt gacatccaaa atctgaaatg agaaatgctc caaaaactga 720
aactttttca atgccgacac gatgctcaa gaaaatgcta attggagcat ttcagatttt 780
ggatttttgg atttgggatg ctcaactggc ataatgtgaa tattccaaac tctgaaaaaa 840
tctgaagtct aaaaacttct tggctctcaag gattttggat aaaggatact caatgtgcaa 900
catgtagaat ggtggttgca aggtgggagg agagaatgga gagttactgt ttaatgatac 960
aatgtttccg tttgggaaga tggaaagtgt tggagatgtg tgatgggtat ggttgcgcaa 1020
caatgggaag gtacttagta ctgcttaact gtgcacactt aaaaatggta aaaatgataa 1080
attttgtgta tgtcttaaaa caataaaaga agttttttaa aaaaaaaaaa 1130

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<210> 215

<211> 1273

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2061933

<400> 215

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ttgggtttta agttcctttg gtccagggaa ggggtccaagc agccacagtt gccctaaatc 180
tccatcatta agtcttccag caagggttaag tgcagtatgg aaggagaagg ggggaagagga 240
cggtaacggc cccacactcc aggtcgagaa agagtaatta ggaggcctga ggaggggccc 300
aggaaaggct gttgggggtg gctgggggtg gtacccgagc gccttcccct cacctcaacc 360
agagaagagc atccgggttg tttttaaaagc ttttagcctg ccctagcaag gacaaagcat 420

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gtttagattag agatgcttct gctgatcgca ggggttctta tttgaaaaca tctatgatgg 480
gggtgggggtg ggaggagaca ggttggtggtt atgcaggaaa atcttgtcct aaaaatatat 540
gagtttgggg gtaaggggtg ggatagccaa gcaaaatcag taattatattt aaaatgaaca 600
tatgtattttt tattaacttt tagttaaata cagattttac aacgagggtca gcataagcct 660
aaatctatat agaggggctaa ctcaggcatt gtcttggtta tttgtagact ggattaaaaa 720
caacctgtcc tgttttgtca gttcccagct tcttcgttta gaataaatta gaccaaaaga 780
agaaacgtgc ttgtctctgt ataccgcag aatgaagtta ctggtgttaa aactggattt 840
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tctctttatg ttgtttctct tctgagtcat ggtaaaacaa taaattatca tctctaggtg 1260
gaaaaaaaaa aaa 1273
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<210> 216

<211> 1279

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2081422

<400> 216

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cactcattcc ctttctctct cccccacccc ttcttccctt cactttcttc ctttctctac 180
ttctcctttc cctctgtgct agagctcttg gcaccagtca agctgtccca cccctcaggg 240
cctctcagct gactgatgcc catggctccc tctctctaca cccaaagacc ctggcttgcc 300
catgtctctg atgagaattc aaagggagct gtgtttatat aacgtagagg gatttacctg 360
tggtttttcc tttactcact tctcaaaac tgtacattta tggcatagga tgtcagtcct 420
aaaagtttta ttatcaaaac agtaggtggc aagtaattat tatcataaat ccagcaggtt 480
ctagagaagc caagttggag gagaaagcag gatagagtc accatgacca ttgattggtg 540
ggcacattct ttctaagaaa cagattaatt ccattgtatc tgttctctgt tatcccatc 600
cagcttatga ttagagtctt gagctcaca cttggctctc taagaggtag tcagtgggtc 660
gcgttccagc ttgaccacag cgttttggtt tttctttaag tgttgtgttg taatgcttg 720
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ccttaactat ctgaactctt cctgtcctgt aagactgagc tcaactggca tatectatag 960
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atcacataaa ctacatatat aaagcttcta gcttagtaaa ctctaaatgt gtttttttaa 1260
actaaagaat gagggggggg 1279
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<210> 217

<211> 899

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2101278

<400> 217

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cccatgagca ggaccgcctc catgattggg gagcatgcac ttgtgactgc agggtaagag 120
tgggaagata ggtttgtgga gtggcaccga caggactgtg attgtgtgtg ggctgcccc 180
acatttctct gggggatgct tatgtgagag tgggcccagt gaaagagtta ccaagccacc 240
cacacccta acactgttct ggatgagaga tgagagcaga ccggcttctc cccatcagtg 300
cattgtgcct gttgtacacc cctggaggag ccctggagcc agcccagggt ggggtacacaa 360
tcttttttaa ttccatatgg ttgccagctt atttctttca cttgtttact gtaatatctg 420
gcgtgttttt atttatctaa ttttgtattc agttataacc atggtagggg tagtgaatat 480
atgacagggtg taatccctgg tgctgcagtg gaccttcttt tcttttggac aagataatac 540
tgtgagtttc cctccttctc tccctctaatt ttgttttctt tttttcccca gcctcttgca 600
tccccttctt ttctaccctg tccatacaact atcatatgca cagtcttctc tctttgtgtg 660
tgactgttac aaaatttcac ttttcaaaat cgaaatcagg tgtttgctca aatgagggga 720
gatttttttt tttttttttt ttttaaattg tgagacttca gcagagtact ttcttttgg 780
tggtttcccc caaaaaccca tcagtctggg agagcattgg gagtggaaat catgttgctt 840
gggatgctgg tttctttgaa aattatataa aacgtatgta aaaggtcccc ccatttggg 899

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<210> 218

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2121353

<400> 218

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caaagtgtg ggattacagg tatgagccac cgcaccgggc ctgttctatt tttctagtta 60
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ccccggcttt tcccaggcag gctcctgcgt gccactggc tccagcctgg tectctgtct 180
cttggtgtgt tcaactctgc tctttgtccc gactctggcc ctgcttacag gggccactac 240
ctgctgggtg ctccataaca agcgtctggc gttgagaccc ctggcatggc aggggctttg 300
gggtctggtt tccacaaggc ttagccatgg cagaacctcg ttttatttta actctttgcc 360
cctacaaaca aacagcagta cttgccagaa ccattcttgg gattcaggag ctggggcgac 420
tgccttggcc tctggccgca cccaggaggg tggggttggg tctgtgtagt tgccaggccc 480
acacctgcca gcagggggct gactggatcc atgctttact gtgtttaatg ggggtaacag 540
gggtccctac agccctccca gctaaacatt tggaaacaaa caccagccct tttgtagtgg 600
atgcagaata aaattgttaa tccaatcacc tccaaaaaaa aaaaa 645

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<210> 219

<211> 703

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2241736

<400> 219

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ccacgcgtcc gctgtaaacc agaaaaatgt tggttatcta gaaaacttga gagagcatgt 60
agattaaact ttctcttttg agttctaaaa cattaactgg aaagattaga taatatacta 120
aatgtatata gaagtataca gactatacaa agactgaaac aagtcccttt tgcaactaaa 180

```



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ctctataaca ttaccgcaga aatttttggtt ctatgtagca tggacctcct aaggaattct 240
gtttctttta gcattgagat ccctgggtgct ctttttttac ctcagaattg gtacaatcat 300
tattaaacgt taatttatatt caaactttttt aattgaaaaa aggaaagggga aacttaattg 360
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tgagttagaa tctctaggta tagggcccag gtatctgcat ttccacagggt ttcttgragg 600
tgactttctg caagctaaag tatgagaacc attggcttgg atgtagttct aaacttttag 660
gtctgtaaat cttgaaatct tgaactgaag gtcaactatt ggc 703

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<210> 220

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2271935

<400> 220

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aaatgaccct cctcctccac tcctcttcgc ttctctcatt tgctaaagtg gtcctttctc 120
tgctgaaat caggcccttt ggtgatggaa atttttagctt aaagcagagt tctaagcaga 180
atcctaacc tgcgagggtg gggagaaaat caatgttttg agctgggtgc tgtttgcagc 240
gaggtgctgg tgaggccatt ttcatacagga ggaacggtgg tgggtggctac ttctgggctt 300
tagatccacg caaggctctcc taaatacaag tcaactgtcat ggtacacaat ttagcaaaac 360
ttggaggctg attttccccg ttgacttagc tagggtcagg aggaagctgt ttagaagtac 420
agaggttctg catctgggag ggtaaaatcc aaacgcctct catgctcaga gggaaagcat 480
gcctgcatgt ttactatcac tgctggccta cgtgcttgtg tgctgaattt agatgg 536

```

<210> 221

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2295344

<400> 221

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ttgacgtttt cttataatga gttttttctt ataattttta atttatgctg taatgtttct 120
tatttacaat gttatctctt aaatctttga gtacattaca ttttctcccc tgataatctc 180
ttctaaatta ctttctctag ttggttttct tcccttcctt aatgttagcc attcttcagg 240
tgaagggtta tcctcaatgt actcttcatt ttttaagggga ggggtctaaaa ccttgtgggt 300
aggacttacc aacggagttt cattgcatga tgatcttatt gagcttattg gtagccctta 360
tctcagtatc tttagttttt cttgggctgg tcagattttc aagagaagac ttttcatttc 420
ctttgtggag ggaaaaggcc ttttaccagc actcttcaag ctcagtaggg gaaagacttc 480
aagcactcag gaagcatgca ttcactttat ttggaacaat acccttactt gtaactgtgc 540
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tggtggggta acaaaaagtg tggagctgaa gaggtacct ataaatgaag ttgttttctg 660
gccgggcgca gtggctcacg cctgtaatcc cagcacttcg ggaggccaag gtggagggat 720
cacttgagtc caggagtttg agaccagcct gggcaacata ctgagactcc gtctctccaa 780
aaaaaaaaa

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<210> 222
 <211> 1045
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2303994

<400> 222
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 tttgaagatg gaacaggaaa ctagagtgc tttaaaatac tctgtcttca ttttaacatg 180
 ttgaatggaa taactgcata tcaccatgag ttgtttttgc ttttcataca gacttgtatg 240
 tgtcatttga gtggtttcca gattggagcg aggttattct gatctaaatg aacagcattt 300
 ttttccttag cctctgtttg ccactctggg tatctctcct atgggcaaag ccattagaaa 360
 tgcataaaac ctcgagacat ggtttttggc aaaaactcca tgactttaaa ctagctcttt 420
 tactactgac ctttcacaga gaaaaaatat ttcccttgaa aaaaactggg ctgtgcattt 480
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 ttaaaaaaaa aaaaaaagat tttggagact accagggtaa gattccaact tgtccaaaag 600
 ctttctggcc ttacatattt tattataaaa attctcaagt ctggtaatct tctatgtcag 660
 agctagtgat ttcaaaaggt ttcacaattc cccaagacaa aagtgatttt cgttcattat 720
 aataagggtta agtgatatgt gattcataac aattttgatg tgaagaaggg aaggacatca 780
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 gacaccgtgg attgaccttc ccgggtccac taatataaag ccaataaagc ttaaaaaacac 960
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<210> 223
 <211> 553
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2497805

<400> 223
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 ccaggcacag cagttggtga ctccctgggt ggagccgtgt cccaccgggt cctgatactg 180
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 tcatttgggt ttgctttttt tgtttgtttg ttttcaccta atttttgcca gacttaagct 480
 agttttgctg ctttttgaag ctagtggag aatcatttta ttccctgggga taatttgggg 540
 gcttttgaat cca 553

<210> 224
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2646362

<400> 224
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ttggtgtgtg tgagctggtg ggtgccacat atttggggat ttgaagaagg aggtgagatg 660
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<210> 225
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221>
<222> 492
<223> a or g or c or t, unknown, or other

<220>
<221> misc_feature
<223> Incyte Clone No: 2657146

<400> 225
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tgatctgtca atgtttaagg ctgttggtgg ttcttgtagc tttgctaata tgtttttctc 180
ctgacagggt aacctgccct cttaactcag cagtgggtct agcgtcctat gccgtacaat 240
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atgttagatt aaggaagggt gttaaagggg aaagaatgaa tgaactgtgg tgtgaaattt 480
cttccaagga gnccatccga cagcagaca 509

<210> 226
<211> 2153
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2755786

<400> 226
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ccatgggccc gcttgaggca cactgagggg acgcggggct gggccatggc cggcgctcgg 120

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gccgccgccg cccgtgcctc ggccgggggtcc tcggcctctt caggcaacca gccgcctcag 180
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gaagggtctca tatttaactg gaagcaggac tacgttgatg ccccatgag catccccgac 960
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<210> 227

<211> 791

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2831245

<400> 227

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tgagggtgggt ggatcacctg aggtcagaag ttcgagaaca gcctagccaa catggcgaaa 600
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<210> 228

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3116250

<400> 228

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<210> 229

<211> 764

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3129630

<400> 229

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acaaggcaga actaggggac ttgaccttg gacctttttg ggtcctaaac tccaggtaag 660
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<210> 230
<211> 540
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 007632

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<210> 231
<211> 857
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1236968

<400> 231
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<210> 232
<211> 1010
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 1334153

<400> 232

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<210> 233

<211> 1981

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1396975

<400> 233

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gccatcaaca gtgtatactt ctggagcctt ctactgataa acagaggccc cagaagacga 1560
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1981

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<210> 234

<211> 744

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1501749

<400> 234

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gaggtgcagc agtggtacca gcagtttctc tacatgggct ttgacgaagc gaaatttgaa 360
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744

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<210> 235

<211> 979

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1575240

<400> 235

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gaagcagcta tgaggatgca gcagccttct gttaagccag gctttaagga tctgcaaaaa 840
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<211> 760

<212> DNA

<213> Homo sapiens

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<223> Incyte Clone No: 1647884

<400> 236

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<210> 237

<211> 1080

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1661144

<400> 237

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<210> 238

<211> 1129

<212> DNA

<213> Homo sapiens

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<223> Incyte Clone No: 1685409

<400> 238

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<210> 239

<211> 2370

<212> DNA

<213> Homo sapiens

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<221>

<222> 122, 124

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<220>

<221> misc_feature

<223> Incyte Clone No: 1731419

<400> 239

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```
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<210> 240

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2650265

<400> 240

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cctggtctct gttcccttcc gtactcaaag ctctgtcatc caggaggggg aaaccggaga 180
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ggcgagattc tgggtctgct tagccggtgc tggcttcttt cttgcatttt tgggttttgca 360
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ggataacatc ccaaagatat tagtgttcac agaggatgga tatttccctac gagcctggaa 600
ttatacagtt gacacacctc atggatatatt tgcagccagt actctatatg aacaatccgt 660
ctggatcacg gatgtaggaa gtggatgtga tagtaatatc tattaaatta tcttactgga 720
```

```

aatcacatct ttgcacatgt ccttggtttgt attgttttaa atcagagttg ctgaatctaa 780
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ctgtggaatt aagaaattta acaagggctg gacgcctg gcacgcctgt aatcccagca 900
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acggtgaaac ccccgctctc a
981

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<210> 241
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2677129

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<400> 241
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tgccttactg ctattaatta attttttttt ggtctctttc ttcttgctt accctttgtt 180
taacaaccaa atcaactcta gatcaatgaa tgaaataaaa aatctccagt acctacctcg 240
gaccagtga ccccgcgagg ttctctttga agataggact agagctcatg ctgatcatgt 300
cggtcagggg ttgtactggc agagtacggc tgctgttggg gttttgaaag ctgtacaatt 360
tggtgaatgg agtgaccaac ctgcataaac caaagatgtg atttgttttc atgctgagga 420
ttttactgat gttgtacaaa gacttcagtt agatcttcat gaacctccag tttccagtg 480
cgtacagtgg gtagatgaag ctaaactaaa ccaaagagg cggaaggca ttcgttatgc 540
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cacaaatgtc agcatattct tttacacaga tatgcaagtt agagtgtatc tatccggtag 1140
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cgag
1204

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<210> 242
 <211> 784
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 3151073

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<400> 242
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cccattctcg agcccctcag ctttataggg atgtcagctt ggccccaatg tagtccatt 180
tacagccaga ctccctggact tgccctatgag ccattctcat ttccaaaaag gcgatattgg 240
gtatgtacat tgcattgaaat aaagtgggaa tgtcccagaa gcagaaggac atctgatgca 300
gtccacgcca ataaattggg cttaccttta aaaatcatct gaatatgcag gtcttagggc 360
agagaatata gacagcttaa gattttctaa actacaagtc ccacccaaaa tacggtattt 420

```

```

tcatgatttc ccaaagggtg accatcagca agactggata tttttcagac ttaagatgac 480
tgttcagtag ctgatgttct ggaaaagatc tgggccttca ccatgaaatc ttaaagtgtga 540
gcagttactg gatgttgaat ttgaaaccta ttcatttctt tttttaaaac aagcttggtc 600
atctctgtgc aatgctataa ttcggaacga aacaaagcac aatgttaata aggtagacac 660
taattcattc ctctgaagag agatctcttc cagacatttt aagccagggc aagaaatgtt 720
taaagatgtt ttctgcagtt gccgtagaaa cactccttag cagtcattct ggctgttggt 780
aaaa

```

<210> 243

<211> 426

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3170095

<400> 243

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ctccattaaa ccaccaccag ctccccaagc cacccttca gccatgaagt tctgtctct 60
ggtcttggca gccctcggat tcttgacca ggtgatcca gccagtgcag gtgggtcaaa 120
atgtgtgagt aacaccccag gatactgcag gacatgttgc cactgggggg agacagcatt 180
gttcattgtc aacgcttcca gaaaatgctg catcagctac tcttctctgc cgaagcctga 240
cctaccacag ctcatcggtg accactggca atcaaggaga agaaacacac aaaggaaaaga 300
caagaagcaa caaacgaccg taacatcata ataaccactg ctatcgctc caccaactca 360
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<210> 244

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221>

<222> 1651, 1655

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 3475168

<400> 244

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ccagcacag cgctgtcca ggacaagtgc ccagtaaaca cttgggaagc aatgcaagcg 180
tcttccacag agctcctgca aacagacccc cgacccaagc ctttctctct gcctccactg 240
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cctctccaca ctacagccaga gggagctatt aaaactgcgg gccagcccac atcagtccac 360
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gacttcttcc tgagcaagggt agggctcttc tacctagtca tgagggcagg gatttttgtc 720
tggtgtgttc tctgtgtgccc ccagtgcca tccagtgccc tggcagatgg taagtgtctg 780

```

```

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```

<210> 245

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 3836893

<400> 245

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accagctaaa aaaaaaaa

```

918

<210> 246

<211> 676

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 4072159

<400> 246

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gtgctgctcc caaaacccca aagcaagcat ggaagagcag accaactcca gaggaaatgg 180
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taaagggagc aggcaa 676
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<210> 247

<211> 2255

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1003916

<400> 247

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aaagacagca agttgtgtgt gcgcccggga cgcgggaggg aaggtagccg ccgcccgcga 420
gccattggacc atcatcttta gtgcagagga tggaaagtgt atgccagta agactgaaga 480
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ttcagtgttt atgcagacct ttagagttta gcctttgtat ttccatgtta ttccacaata 1980
tgcaatatatt ctctgagtag cttctgctat gatattctta tgaagaaaag gggcaacttt 2040
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ctgtccacta taggagagaa ttcagccgaa gatatgagag taatgagaga cattttccag 2100
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2255

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<210> 248

<211> 1223

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2093492

<400> 248

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cactgatgca gctctctatg gattgccctt gtgacctggc agatgggctg aagggtgtcc 240
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1223

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<210> 249

<211> 1188

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2108789

<400> 249

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<210> 250

<211> 1792

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2171401

<400> 250

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<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2212530

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<210> 252
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte Clone No: 2253036

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<210> 253

<211> 3775

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2280161

<400> 253

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<210> 254

<211> 1856

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte Clone No: 2287485

<400> 254

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<213> Homo sapiens

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<211> 1671

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2383171

<400> 256

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<213> Homo sapiens

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<223> Incyte Clone No: 2484813

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<223> Incyte Clone No: 2495719

<400> 261

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47, C12N 15/11, C12Q 1/68, C07K 16/18, G01N 33/68, A61K 38/17</p>	A3	<p>(11) International Publication Number: WO 00/00610</p> <p>(43) International Publication Date: 6 January 2000 (06.01.00)</p>																																			
<p>(21) International Application Number: PCT/US99/14484</p> <p>(22) International Filing Date: 25 June 1999 (25.06.99)</p> <p>(30) Priority Data:</p> <table style="width: 100%; border: none;"> <tr> <td style="width: 40%;">60/090,762</td> <td style="width: 40%;">26 June 1998 (26.06.98)</td> <td style="width: 20%; text-align: right;">US</td> </tr> <tr> <td>60/094,983</td> <td>31 July 1998 (31.07.98)</td> <td style="text-align: right;">US</td> </tr> <tr> <td>60/102,686</td> <td>1 October 1998 (01.10.98)</td> <td style="text-align: right;">US</td> </tr> <tr> <td>60/112,129</td> <td>11 December 1998 (11.12.98)</td> <td style="text-align: right;">US</td> </tr> </table> <p>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications</p> <table style="width: 100%; border: none;"> <tr> <td style="width: 40%;">US</td> <td style="width: 40%;">60/090,762 (CIP)</td> <td style="width: 20%;"></td> </tr> <tr> <td>Filed on</td> <td>26 June 1998 (26.06.98)</td> <td></td> </tr> <tr> <td>US</td> <td>60/094,983 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>31 July 1998 (31.07.98)</td> <td></td> </tr> <tr> <td>US</td> <td>60/102,686 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>1 October 1998 (01.10.98)</td> <td></td> </tr> <tr> <td>US</td> <td>60/112,129 (CIP)</td> <td></td> </tr> <tr> <td>Filed on</td> <td>11 December 1998 (11.12.98)</td> <td></td> </tr> </table> <p>(71) Applicant (for all designated States except US): INCYTE PHARMACEUTICALS, INC. [US/US]; 3174 Porter Drive, Palo Alto, CA 94304 (US).</p>	60/090,762	26 June 1998 (26.06.98)	US	60/094,983	31 July 1998 (31.07.98)	US	60/102,686	1 October 1998 (01.10.98)	US	60/112,129	11 December 1998 (11.12.98)	US	US	60/090,762 (CIP)		Filed on	26 June 1998 (26.06.98)		US	60/094,983 (CIP)		Filed on	31 July 1998 (31.07.98)		US	60/102,686 (CIP)		Filed on	1 October 1998 (01.10.98)		US	60/112,129 (CIP)		Filed on	11 December 1998 (11.12.98)		<p>(72) Inventors; and (75) Inventors/Applicants (for US only): LAL, Preeti [IN/US]; 2382 Lass Drive, Santa Clara, CA 95054 (US). TANG, Y., Tom [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). GORGONE, Gina, A. [US/US]; 1253 Pinecrest Drive, Boulder Creek, CA 95006 (US). CORLEY, Neil, C. [US/US]; 1240 Dale Avenue #30, Mountain View, CA 94040 (US). GUEGLER, Karl, J. [CH/US]; 1048 Oakland Avenue, Menlo Park, CA 94025 (US). BAUGHN, Mariah, R. [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). AKERBLOM, Ingrid, E. [US/US]; 1234 Johnson Street, Redwood City, CA 94061 (US). AU-YOUNG, Janice [US/US]; 1419 Kains Avenue, Berkeley, CA 94702 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). PATTERSON, Chandra [US/US]; 490 Sherwood Way #1, Menlo Park, CA 94025 (US). REDDY, Roopa [IN/US]; 1233 W. McKinley Drive, Sunnyvale, CA 94086 (US). HILLMAN, Jennifer, L. [US/US]; 230 Monroe Drive #12, Mountain View, CA 94040 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Mountain View, CA 94043 (US).</p> <p>(74) Agents: BILLINGS, Lucy, J. et al.; Incyte Pharmaceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report.</i></p> <p>(88) Date of publication of the international search report: 29 June 2000 (29.06.00)</p>
60/090,762	26 June 1998 (26.06.98)	US																																			
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US	60/112,129 (CIP)																																				
Filed on	11 December 1998 (11.12.98)																																				
<p>(54) Title: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS</p> <p>(57) Abstract</p> <p>The invention provides human signal peptide-containing proteins (HSPP) and polynucleotides which indentify and encode HSPP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of HSPP.</p>																																					

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DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

Intern. Application No.
PCT/US 99/14484

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 C12N15/11 C12Q1/68 C07K16/18
G01N33/68 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	HUDSON T.: "Human STS." EMBL DATABASE ENTRY HS578357, ACCESSION NUMBER G22578, 1 June 1996 (1996-06-01), XP002125359 abstract	5
A	--- TASHIRO K. ET AL.: "SIGNAL SEQUENCE TRAP: A CLONING STRATEGY FOR SECRETED PROTEINS AND TYPE I MEMBRANE PROTEINS" SCIENCE, vol. 261, 1993, pages 600-603, XP002911163 ISSN: 0036-8075 the whole document	1-16, 19
A	--- EP 0 607 054 A (HONJO TASUKU ;ONO PHARMACEUTICAL CO (JP)) 20 July 1994 (1994-07-20) the whole document --- -/-	1-16, 19

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *&* document member of the same patent family

Date of the actual completion of the international search

20 December 1999

Date of mailing of the international search report

05. 04 2000

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Mandl, B

INTERNATIONAL SEARCH REPORT

Inter. Application No
PCT/US 99/14484

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	JACOBS K. A. ET AL: "A genetic selection for isolating cDNAs encoding secreted proteins" GENE, vol. 198, 1997, pages 289-296, XP002102962 ISSN: 0378-1119 the whole document	1-16,19
A	WALLIN E. ET AL.: "Properties of N-terminal tails in G-protein coupled receptors: a statistical study" PROTEIN ENGINEERING, vol. 8, no. 7, 1995, pages 693-698, XP002102961 ISSN: 0269-2139 the whole document	1-16,19

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 14484

Box I Observations where certain claims were found unsatisfactory (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 19 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 17, 18, 20
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see additional sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Further defect(s) under Article 17(2)(a):

Continuation of Box 3.

Claims Nos.: 17,18,20

Claims 17,18 and 20 refer to antagonists and agonists of the polypeptides without giving a true technical characterization. Moreover, no such specific compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6, PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of, claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

INVENTION 1: Claims 1-20 (all partially)

A polypeptide comprising the amino acid sequence of SEQ.ID.1 and variants having at least 90% amino acid sequence identity therewith; the polynucleotide encoding said polypeptide (as represented by SEQ.ID.135) and variants having at least 90% sequence identity with said polynucleotide; a polynucleotide that hybridizes therewith or a polynucleotide that is complementary thereto; a method for detecting said polynucleotide, an expression vector comprising said polynucleotide; a host cell comprising said vector; a method for producing said polypeptide; a pharmaceutical composition comprising said polypeptide; a purified antibody, agonist or antagonist specific for said polypeptide; and a method for treating or preventing a disorder associated with decreased or increased expression of said polypeptide.

INVENTIONS 2-134: Claims 1-20 (all partially)

Idem as subject 1 but limited to one DNA sequence selected from SEQ.IDs. 136-268 at a time and the corresponding polypeptide, where invention 2 is limited to SEQ.IDs. 136 and 2, invention 3 is limited to SEQ.IDs. 137 and 3, and invention 134 is limited to SEQ.IDs. 268 and 134.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/14484

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0607054 A	20-07-1994	CA 2113363 A	15-07-1994
		JP 2879303 B	05-04-1999
		JP 6315380 A	15-11-1994
		JP 11308993 A	09-11-1999
		US 5525486 A	11-06-1996
